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<110> Odyssey Thera, Inc.
Michnick, Stephen
MacDonald, Marnie
Lamerdin, Jane
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COMPLEMENTATION ACCASE

## <120> FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT COMPLEMENTATION ASSAYS

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<301> Zhang, J. et al

<302> Creating new fluorescent probes for cell biology

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Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                                105
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
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Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
Pro Val Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
                    150
                                        155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
                                185
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
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Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
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                                     170
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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                                    90
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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135

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165  $\phantom{0}$  170  $\phantom{0}$  175

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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205

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Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val 35 40 45

Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala 50 60

Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Val 65 70 75 80

Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser 85 90 95

Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr

Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly
115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn

130 135 140

Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile 145 150 155 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg 185 Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp 200 Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile Ala Ser Gly Ser Ala Leu Pro <210> 10 <211> 231 <212> PRT <213> Anthozoa zoanthus; <220> <221> misc\_feature <223> Zoanthus ("z") FP538 <300> <301> Matz, M.V. et al <302> Fluorescent proteins from nonbioluminescent Anthozoa species <303> Nat. Biotech. <304> 17 <305> 10 969-73 <306> <307> 1999-\_ <313> (1)..(231) <400> 10 Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr 5 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val 35 40 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser 90

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Val Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly 120 Met Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn 135 Trp Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile 150 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser 185 Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp 195 200 Arg Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile 215 220 Ala Phe Pro Ser Ala Leu Ala 225 230 <210> 11 <211> 232 <212> PRT <213> Anthozoa discosoma; <220> <221> misc\_feature <223> Discosoma striata ("ds") FP483 <300> <301> Matz, M.V. et al <302> Fluorescent proteins from nonbioluminescent Anthozoa species <303> Nat. Biotech. <304> 17 <305> 10 <306> 969-73 <307> 1999-<313> (1)..(232) <400> 11 Met Ser Cys Ser Lys Ser Val Ile Lys Glu Glu Met Leu Ile Asp Leu His Leu Glu Gly Thr Phe Asn Gly His Tyr Phe Phe Ile Lys Gly Lys Gly Lys Gly Gln Pro Asn Glu Gly Thr Asn Thr Val Thr Leu Glu Val Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Cys Pro Gln

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Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser
Met His Phe Glu Asp Gly Gly Leu Cys Cys Ile Thr Asn Asp Ile Ser
Leu Thr Gly Asn Cys Phe Tyr Tyr Asp Ile Lys Phe Thr Gly Leu Asn
Phe Pro Pro Asn Gly Pro Val Val Gln Lys Lys Thr Thr Gly Trp Glu
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                        135
Pro Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Ile Gly Asp
Ile His His Ala Leu Thr Val Glu Gly Gly His Tyr Ala Cys Asp
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Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
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Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
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Phe Lys Ser Ile Tyr Met Ala Lys Lys Ala Pro Val Gln Leu Pro Gly
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Tyr Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp
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Val Lys Met Ala Glu Gly Ala Pro Leu Pro Phe Ser Tyr Asp Ile Leu 50 55 60

Ser Asn Ala Phe Gln Tyr Gly Asn Arg Ala Leu Thr Lys Tyr Pro Asp 65 70 75 80

Asp Ile Ala Asp Tyr Phe Lys Gln Ser Phe Pro Glu Gly Tyr Ser Trp 85 90 95

Glu Arg Thr Met Thr Phe Glu Asp Lys Gly Ile Val Lys Val Lys Ser

Asp Ile Ser Met Glu Glu Asp Ser Phe Ile Tyr Glu Ile Arg Phe Asp 115 120 125

Gly Met Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Leu 130 135 140

Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Val Arg Asp Gly Val Leu 145 150 155 160

Val Gly Asp Ile Ser His Ser Leu Leu Leu Glu Gly Gly Gly His Tyr 165 170 175

Arg Cys Asp Phe Lys Ser Ile Tyr Lys Ala Lys Lys Val Val Lys Leu 180 185 190

Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Leu Asn His Asp 195 200 205

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Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
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Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
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Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
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170

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Met 1	Ala	Ser	Ser	Glu 5	Asp	Val	Ile	Lys	Glu 10	Phe	Met	Arg	Phe	Lys 15	Val	
Arg	Met	Glu	Gly 20	Ser	Val	Asn	Gly	His 25	Glu	Phe	Glu	Ile	Glu 30	Gly	Glu	
Gly	Glu	Gly 35	Arg	Pro	Tyr	Glu	Gly 40	Thr	Gln	Thr	Ala	Lys 45	Leu	Lys	Val	
Thr	Lys 50	Gly	Gly	Pro	Leu	Pro 55	Phe	Ala	Trp	Asp	Ile 60	Leu	Ser	Pro	Gln	
Phe 6	Gln	Tyr	Gly	Ser	Lys 70	Ala	Tyr	Val	Lys	His 75	Pro	Ala	Asp	Ile	Pro 80	
Asp '	Tyr	Leu	Lys	Leu 85	Ser	Phe	Pro	Glu	Gly 90	Phe	Lys	Trp	Glu	Arg 95	Val	
Met .	Asn	Phe	Glu 100	Asp	Gly	Gly	Val	Val 105	Thr	Val	Thr	Gln	Asp 110	Ser	Ser	
Leu (	Gln	Asp 115	Gly	Glu	Phe	Ile	Tyr 120	Lys	Val	Lys	Leu	Arg 125	Gly	Thr	Asn	
Phe	Pro 130	Ser	Asp	Gly	Pro	Val 135	Met	Gln	Lys	Lys	Thr 140	Met	Gly	Trp	Glu	

Ala Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Gl 145 150 155 16	
Ile Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Gl 165 170 175	u
Val Lys Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Al 180 185 190	a
Tyr Lys Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Ty 195 200 205	r
Thr Ile Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gl 210 215 220	У
Ala 225	
<210> 17 <211> 696 <212> DNA <213> Artificial	
<220> <223> "KFP1" a mutated variant of kindling fluorescent protei     m A. sulcata	n asCP fro
<223> "KFP1" a mutated variant of kindling fluorescent protei	n asCP fro
<223> "KFP1" a mutated variant of kindling fluorescent protei m A. sulcata <220> <221> CDS	g 48
<pre>&lt;223&gt; "KFP1" a mutated variant of kindling fluorescent protei     m A. sulcata  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(696)  &lt;400&gt; 17 atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc ga Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Gl</pre>	g 48 u
<pre>&lt;223&gt; "KFP1" a mutated variant of kindling fluorescent protei     m A. sulcata  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(696)  &lt;400&gt; 17 atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc ga Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Gl 1</pre>	g 48 u 96 Y
<pre> &lt;223&gt; "KFP1" a mutated variant of kindling fluorescent protei     m A. sulcata  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(696)  &lt;400&gt; 17 atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc ga Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Gl 1</pre>	g 48 u 96 y 144 y 192

					gag Glu												288
					ctg Leu												336
					aag Lys												384
					cag Gln												432
					gtg Val 150												480
					ggc Gly												528
					aag Lys												576
					cgc Arg												624
					tac Tyr												672
_			_	_	ggc Gly 230												696
<210 <211 <212 <213	2> I	232 PRT	icia	al													
<220 <220	3> '		l" a sulo		ated	vari	lant	of }	cind]	ling	fluc	oreso	cent	prot	ein	asCP	fro
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Met 1	Ala	Ser	Leu	Leu 5	Thr	Glu	Thr	Met	Pro 10	Phe	Lys	Thr	Thr	Ile 15	Glu		
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Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly 35 40 45

Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr 50 55 60

Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr 85 90 95

Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly 100 105 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala 115 120 125

Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr 130 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met 145 150 155 160

Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr 165 170 175

Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
180 185 190

His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly
195 200 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala 210 215 220

Ala Pro Ser Lys Leu Gly His Asn 225 230

<210> 19

<211> 10

<212> PRT

<213> Artificial

<220>

<223> flexible linker

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<222>
      (1)..(114)
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agt aaa gga gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa
                                                                    48
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
               5
tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt
                                                                     96
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
                               25
gaa ggt gat gca aca tac
                                                                    114
Glu Gly Asp Ala Thr Tyr
       35
<210> 21
<211> 38
<212> PRT
<213> Artificial
220>
      modified fragment= GFP F1 (aa 1-39 of wt GFP) w/o. Met @ position
<223>
<400> 21
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
           2.0
                               25
Glu Gly Asp Ala Thr Tyr
       35
<210> 22
<211> 600
<212> DNA
<213> Artificial
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modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1 <223> <220> <221> CDS <222> (1)..(600)<400> 22 atg gga aaa ctt acc ctt aaa ttt att tgc act act gga aaa cta cct 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt gtt caa tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys 20 25 ttt tca aga tac cca gat cat atg aaa cgg cat gac ttt ttc aag agt 144 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 gcc atg ccc gaa ggt tat gta cag gaa aga act ata ttt ttc aaa gat 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 gac ggg aac tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctt gtt aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 aac att ctt gga cac aaa ttg gaa tac aac tat aac tca cac aat gta 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tac atc atg gca gac aaa caa aag aat gga atc aaa gtt aac ttc aaa 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 att aga cac aac att gaa gat gga agc gtt caa cta gca gac cat tat 432 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 480 caa caa aat act cca att ggc gat ggc cct gtc ctt tta cca gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 cat tac ctg tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag 528 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 175 aga gac cac atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190 600 cat ggc atg gat gaa cta tac aaa His Gly Met Asp Glu Leu Tyr Lys

<211> 200 <212> PRT <213> Artificial <220> <223> modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1 <400> 23 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys 25 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 145 155 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185

<210> 23

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<210> 24
<211> 117
<212> DNA
<213> Artificial
<220>
      modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1
<220>
<221>
      CDS
<222> (1)..(117)
<400> 24
gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                    10
                                                                      96
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
ggc gag ggc gat gcc acc tac
                                                                     117
Gly Glu Gly Asp Ala Thr Tyr
<210> 25
<211> 39
<212> PRT
<213> Artificial
<220>
<223> modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
                                25
Gly Glu Gly Asp Ala Thr Tyr
        35
<210> 26
<211>
       600
<212>
       DNA
<213>
      Artificial
<220>
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His Gly Met Asp Glu Leu Tyr Lys

<223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1

<220> <221> CDS <222> (1)((	600)			
			cc acc ggc aag hr Thr Gly Lys	
	ro Thr Leu Val		gc tac ggc ctg ly Tyr Gly Leu 30	
			ac gac ttc ttc is Asp Phe Phe 45	
			cc atc ttc ttc hr Ile Phe Phe 60	
		Ala Glu Val L	ag ttc gag ggc ys Phe Glu Gly 5	
			ac ttc aag gag sp Phe Lys Glu	
Asn Ile Leu G			ac aac agc cac yr Asn Ser His 110	
			tc aag gtg aac le Lys Val Asn 125	
			ag ctc gcc gac ln Leu Ala Asp 140	
cag cag aac ac Gln Gln Asn Th 145	cc ccc atc ggc or Pro Ile Gly 150	Asp Gly Pro Va	tg ctg ctg ccc al Leu Leu Pro 55	gac aac 480 Asp Asn 160
			aa gac ccc aac ys Asp Pro Asn	
Arg Asp His Me	ng gtc ctg ctg et Val Leu Leu 30	gag ttc gtg ad Glu Phe Val Ti 185	cc gcc gcc ggg hr Ala Ala Gly 190	atc act 576 Ile Thr
	ac gag ctg tac sp Glu Leu Tyr			600

<210> 27

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1

<400> 27

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

```
<210>
       28
<211>
       597
<212>
       DNA
       Artificial
<213>
<220>
<223>
       modified frag.; YFPF2A w. F46L mutation
<220>
<221>
       CDS
<222>
       (1)..(597)
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ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg
                                                                       48
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
                            40
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50
                        55
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
                                                                      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat
                                                                      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100
                                105
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc
                                                                      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115
ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae cag
                                                                      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
                        135
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac cac
                                                                      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                         155
                                                             160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
                                                                      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165
                                     170
                                                         175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc gqq atc act ctc
                                                                      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
```

597

ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys

195

<210> 29

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFPF2A w. F46L mutation

<400> 29

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 30 <211> 600 <212> DNA <213> Artificial
<220> <223> modified frag., YFPF2A w. F46L mutation + Met @ postion 1
<220> <221> CDS <222> (1)(600)
<pre>&lt;400&gt; 30 atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15</pre>
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc  144  Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  35  40  45
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag  Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  115  120  125
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac  Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  130  140
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn

145					150					155					160	
cac His																528
cgc Arg																576
ctc Leu															·	600
<210 <211 <212 <213	> 2 > I	31 200 PRT Arti	icia	al												
<220 <223		nodi	Eied	frag	g., ;	YFPF2	2 <b>A</b> v	٧. I	746L	muta	ation	n + N	Met @	oq ©	stion 1	
<400	> 3	31														
Met 1	Gly	Lys	Leu	Thr 5	Leu	Lys	Leu	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val	Pro	Trp	Pro 20	Thr	Leu	Val	Thr	Thr 25	Phe	Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala	Met 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	

Gln Gln Asn Thr 145	Pro Ile Gly 150	Asp Gly Pro	Val Leu Leu Pro 155	Asp Asn 160
His Tyr Leu Ser	Tyr Gln Ser	Ala Leu Ser 170	Lys Asp Pro Asn	Glu Lys 175
Arg Asp His Met 180		ı Glu Phe Val 185	Thr Ala Ala Gly 190	Ile Thr
Leu Gly Met Asp 195	Glu Leu Tyr	Lys 200		
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<220> <221> CDS <222> (1)(59	7)			
			acc ggc aag ctg Thr Gly Lys Leu	
			tac ggc ctg cag Tyr Gly Leu Gln 30	
			gac ttc ttc aag Asp Phe Phe Lys 45	
			atc ttc ttc aag Ile Phe Phe Lys 60	
			ttc gag ggc gac Phe Glu Gly Asp 75	
			ttc aag gag gac Phe Lys Glu Asp	
			aac agc cac aac Asn Ser His Asn 110	
			aag gtg aac ttc Lys Val Asn Phe	

	1	120	125
		Ser Val Gln Leu Al	cc gac cac tac cag 432 la Asp His Tyr Gln 40
			tg ccc gac aac cac 480 eu Pro Asp Asn His 160
			cc aac gag aag cgc 528 ro Asn Glu Lys Arg 175
			cc ggg atc act ctc 576 la Gly Ile Thr Leu 190
ggc atg gac gag Gly Met Asp Glu 195	_		597
<210> 33 <211> 199 <212> PRT <213> Artifici	al		
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	Leu Lys Leu I 5	lle Cys Thr Thr Gl 10	ly Lys Leu Pro Val 15
Gly Lys Leu Thr 1	5	10	- <del>-</del>
Gly Lys Leu Thr  1  Pro Trp Pro Thr 20	5 Leu Val Thr T	10 Thr Leu Gly Tyr Gl 25	15 ly Leu Gln Cys Phe
Gly Lys Leu Thr  1  Pro Trp Pro Thr 20  Ala Arg Tyr Pro 35	Leu Val Thr T Asp His Met L	10 Thr Leu Gly Tyr Gl 25 Lys Arg His Asp Ph	ly Leu Gln Cys Phe 30  he Phe Lys Ser Ala 45  he Phe Lys Asp Asp
Gly Lys Leu Thr  Pro Trp Pro Thr 20  Ala Arg Tyr Pro 35  Met Pro Glu Gly 50	Leu Val Thr T  Asp His Met L  4  Tyr Val Gln G 55	Thr Leu Gly Tyr Gl 25 Lys Arg His Asp Ph 10 Glu Arg Thr Ile Ph	ly Leu Gln Cys Phe 30  he Phe Lys Ser Ala 45  he Phe Lys Asp Asp
Gly Lys Leu Thr  Pro Trp Pro Thr 20  Ala Arg Tyr Pro 35  Met Pro Glu Gly 50  Gly Asn Tyr Lys 65	Leu Val Thr T  Asp His Met L  Tyr Val Gln G  55  Thr Arg Ala G  70	Thr Leu Gly Tyr Gl 25  Lys Arg His Asp Pr 10  Glu Arg Thr Ile Pr 60  Glu Val Lys Phe Gl 75	ly Leu Gln Cys Phe 30  he Phe Lys Ser Ala 45  he Phe Lys Asp Asp 0

Ile Met Ala 115	Asp Lys (	-	Asn Gly 120	Ile Lys	Val Asn 125	Phe	Lys	Ile	
Arg His Asn 130	Ile Glu A	Asp Gly 135	Ser Val	Gln Leu	Ala Asp 140	His	Tyr	Gln	
Gln Asn Thr 145		Gly Asp 150	Gly Pro	Val Leu 155	Leu Pro	Asp .	Asn	His 160	
Tyr Leu Ser	Tyr Gln 8 165	Ser Ala	Leu Ser	Lys Asp 170	Pro Asn		Lys 175	Arg	
Asp His Met	Val Leu 1 180	Leu Glu	Phe Val 185	Thr Ala	Ala Gly	Ile 190	Thr	Leu	
Gly Met Asp 195	Glu Leu S	Tyr Lys							
<210> 34 <211> 600 <212> DNA <213> Arti	ficial								
<220> <223> modi	fied frag	.; YFPF2	A w. F	'46L/F64I	_ mutat:	ions	+ Me	t @ pos	sit. 1
<223> modi <220> <221> CDS	fied frag	.; YFPF2	Aw. F	'46L/F64I	ı mutat:	ions	+ Me	t @ pos	sit. 1
<223> modi <220> <221> CDS	.(600)	ctg aag	ctg atc	tgc acc	acc ggc	aag Lys	ctg	ccc	3it. 1 48
<223> modi <220> <221> CDS <222> (1). <400> 34 atg ggc aag Met Gly Lys	ctg acc cleu Thr 1	ctg aag Leu Lys ctc gtg	ctg atc Leu Ile acc acc	tgc acc Cys Thr 10 ctg ggc	acc ggc Thr Gly tac ggc	aag Lys ctg	ctg Leu 15 cag	ccc Pro	
<223> modi <220> <221> CDS <222> (1).  <400> 34 atg ggc aag Met Gly Lys 1  gtg ccc tgg	ctg acc c Leu Thr 1 5 ccc acc c Pro Thr 1 20	ctg aag Leu Lys ctc gtg Leu Val gac cac Asp His	ctg atc Leu Ile acc acc Thr Thr 25 atg aag	tgc acc Cys Thr 10 ctg ggc Leu Gly	acc ggc Thr Gly tac ggc Tyr Gly gac ttc	aag Lys ctg Leu 30	ctg Leu 15 cag Gln aag	ccc Pro tgc Cys	48
<223> modi  <220> <221> CDS <222> (1).  <400> 34 atg ggc aag Met Gly Lys 1  gtg ccc tgg Val Pro Trp  ttc gcc cgc Phe Ala Arg	ctg acc c Leu Thr 1 5 ccc acc c Pro Thr 1 20 tac ccc c Tyr Pro 1	ctg aag Leu Lys ctc gtg Leu Val gac cac Asp His	ctg atc Leu Ile acc acc Thr Thr 25 atg aag Met Lys 40 cag gag	tgc acc Cys Thr 10 ctg ggc Leu Gly cgg cac Arg His	acc ggc Thr Gly tac ggc Tyr Gly gac ttc Asp Phe 45 atc ttc	aag Lys ctg Leu 30 ttc Phe	ctg Leu 15 cag Gln aag Lys	ccc Pro tgc Cys tcc Ser	48
<223> modi  <220> <221> CDS <222> (1).  <400> 34  atg ggc aag  Met Gly Lys 1  gtg ccc tgg  Val Pro Trp  ttc gcc cgc  Phe Ala Arg  35  gcc atg ccc  Ala Met Pro	ctg acc c Leu Thr 1 5 ccc acc c Pro Thr 1 20 tac ccc c Tyr Pro 2 gaa ggc t Glu Gly 1 tac aag a Tyr Lys 1	ctg aag Leu Lys  ctc gtg Leu Val  gac cac Asp His  tac gtc Tyr Val 55  acc cgc	ctg atc Leu Ile  acc acc Thr Thr 25  atg aag Met Lys 40  cag gag Gln Glu  gcc gag	tgc acc Cys Thr 10 ctg ggc Leu Gly cgg cac Arg His cgc acc Arg Thr	acc ggc Thr Gly  tac ggc Tyr Gly  gac ttc Asp Phe 45  atc ttc Ile Phe 60  ttc gag	aag Lys ctg Leu 30 ttc Phe	ctg Leu 15 cag Gln aag Lys aag Lys	ccc Pro tgc Cys tcc Ser gac Asp	48 96 144

85		90	95
aac atc ctg ggg cac aa Asn Ile Leu Gly His Ly 100		Asn Tyr Asn Ser H:	
tat atc atg gcc gac aa Tyr Ile Met Ala Asp Ly 115			
atc cgc cac aac atc ga Ile Arg His Asn Ile G 130			
cag cag aac acc ccc at Gln Gln Asn Thr Pro I 145			
cac tac ctg agc tac ca His Tyr Leu Ser Tyr G 165			
cgc gat cac atg gtc ct Arg Asp His Met Val Le 180			ly Ile Thr
ctc ggc atg gac gag ct Leu Gly Met Asp Glu Le 195			600
<210> 35 <211> 200 <212> PRT <213> Artificial			
<220> <223> modified frag.;	YFPF2A w. F4	6L/F64L mutations	s + Met @ posit. 1
<400> 35			
<pre>&lt;400&gt; 35  Met Gly Lys Leu Thr Le 1 5</pre>	eu Lys Leu Ile	Cys Thr Thr Gly Ly	rs Leu Pro 15
Met Gly Lys Leu Thr Le		10	15 eu Gln Cys
Met Gly Lys Leu Thr Le	eu Val Thr Thr 25	Leu Gly Tyr Gly Le	15 eu Gln Cys )
Met Gly Lys Leu Thr Leg 5  Val Pro Trp Pro Thr Leg 20  Phe Ala Arg Tyr Pro As	eu Val Thr Thr 25 sp His Met Lys 40	Leu Gly Tyr Gly Le 30 Arg His Asp Phe Ph 45	15 eu Gln Cys ) ne Lys Ser

Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
<210 <211 <212 <213	L> 5 2> I	36 597 DNA Artif	ficia	al												
<220 <223		nodif	fied	frag	J.; 3	/FPF2	2 <b>A</b> v	vith	F64	lL mi	ıtati	ion				
<220 <221 <222	.> (	CDS (1)	. (597	7)												
	aag										ggc Gly					48
											ggc Gly					96
											ttc Phe					144
atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	192

i e	Met	Pro 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Ārg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp		
									gtg Val									240
									atc Ile									288
									aac Asn 105									336
									ggc Gly									384
									gtg Val									432
									ccc Pro								·	480
									agc Ser									528
									gtg Val 185							ctc Leu		576
			gac Asp 195						•									597
	<210 <211 <212 <213	1> : 2> :	37 199 PRT Arti	ficia	al													
	<220 <220		nodi	fied	frag	g.; S	YFPF2	2 <b>A v</b>	vith	F64	lL mi	ıtat:	ion					
	<400	0> 3	37															
·	Gly 1	Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val		
	Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Leu 25	Gly	Tyr	Gly	Leu	Gln 30	Cys	Phe		
	Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala		

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 38 <211> 600 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1 <220> <221> CDS <222> (1)..(600) <400> 38 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

55

50

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30

```
ttc qcc cqc tac ccc qac cac atq aaq cqq cac qac ttc ttc aaq tcc
                                                                     144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                     240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
                                105
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
ate ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae
                                                                     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ccc gac aac
                                                                     480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                    150
                                        155
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                     528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
ege gat cae atg gte etg etg gag tte gtg ace gee geg gte act
                                                                     576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
           180
                                185
                                                    190
ctc ggc atg gac gag ctg tac aag
                                                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
<210> 39
<211> 200
<212> PRT
<213> Artificial
<220>
<223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1
<400> 39
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
                                    10
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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 40

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation

<220>

<221> CDS

<222> (1)..(597)

<400> ggc a Gly I 1	aag															48
ccc t Pro I																96
gcc c Ala A																144
atg o Met F	ccc Pro 50	gaa Glu	ggc Gly	tac Tyr	gtc Val	cag Gln 55	gag Glu	cgc Arg	acc Thr	atc Ile	ttc Phe 60	ttc Phe	aag Lys	gac Asp	gac Asp	192
ggc a Gly A 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240
gtg a Val A																288
atc c Ile I	tg	999 999	cac His 100	aag Lys	ctg Leu	gag Glu	tac Tyr	aac Asn 105	tac Tyr	aac Asn	agc Ser	cac His	aac Asn 110	gtc Val	tat Tyr	336
atc a Ile M	atg 1et	gcc Ala 115	gac Asp	aag Lys	cag Gln	aag Lys	aac Asn 120	ggc Gly	atc Ile	aag Lys	gtg Val	aac Asn 125	ttc Phe	aag Lys	atc Ile	384
cgc c Arg H																432
cag a Gln A 145	aac Asn	acc Thr	ccc Pro	atc Ile	ggc Gly 150	gac Asp	ggc Gly	ccc Pro	gtg Val	ctg Leu 155	ctg Leu	ccc Pro	gac Asp	aac Asn	cac His 160	480
tac c Tyr L	etg Jeu	agc Ser	tac Tyr	cag Gln 165	tcc Ser	gcc Ala	ctg Leu	agc Ser	aaa Lys 170	gac Asp	ccc Pro	aac Asn	gag Glu	aag Lys 175	cgc Arg	528
gat c Asp H	cac His	atg Met	gtc Val 180	ctg Leu	ctg Leu	gag Glu	ttc Phe	gtg Val 185	acc Thr	gcc Ala	gcc Ala	ggg Gly	atc Ile 190	act Thr	ctc Leu	576
ggc a Gly M																597
<210><211><211><212><213>	• 1 • P	1 99 RT rtif	icia	ıl												

<220>

<223> modified frag.; YFPF2A with K79R mutation

<400> 41

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 42

<211> 600

<212> DNA

<213> Artificial	
<220> <223> modified frag.; YFPF2A with K79R mutation + Met @ posit.	L
<220> <221> CDS <222> (1)(600)	
<pre>&lt;400&gt; 42 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>	48
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30	96
ttc gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser 35 40 45	144
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	192
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110	336
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys	600

195 200

<210> 43

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation + Met @ posit. 1

<400> 43

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

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<210> 44
<211> 597
<212> DNA
<213>
      Artificial
<220>
<223>
      modified frag.; YFPF2A with Y66F mutation
<220>
<221>
      CDS
<222>
       (1)..(597)
<400> 44
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg
                                                                       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc ttc
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
                            40
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50
                        55
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
                                                                      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat
                                                                      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc
                                                                      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115
                            120
cgc cac aac atc gag gac ggc aqc gtq caq ctc gcc gac cac tac caq
                                                                      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac
                                                                      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                        155
                                                             160
```

Leu Gly Met Asp Glu Leu Tyr Lys

528

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

165	170	175

gat ca Asp Hi																576
ggc at Gly Me	et i															597
<210><211><212><213>	P	99 RT	icia	al												
<220> <223>	m	odif	ied	fraç	y.; }	/FPF2	2A v	vith	Y66	SF mu	ıtati	lon				
<400>	4	5														
Gly Ly 1	/S	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	
Pro Ti	rp i	Pro	Thr 20	Leu	Val	Thr	Thr	Phe 25	Gly	Phe	Gly	Leu	Gln 30	Cys	Phe	
Ala Aı	_	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met Pi 50		Glu	Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	
Gly As	sn '	Tyr	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val As	sn .	Arg		Glu 85		Lys	Gly		Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile Le	eu (	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile Me		Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Val	Asn 125	Phe	Lys	Ile	
Arg H:	is . 30	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln As 145	sn '	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 46 <211> 600 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A with Y66F mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 46 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly . 85 95 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115

432

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 160

cac tac cto	g agc tac ı Ser Tyr 165	Gln Ser	gcc ctg Ala Leu	agc aaa Ser Lys 170	gac ccc Asp Pro	aac gag Asn Glu 175	aag 528 Lys
cgc gat cac Arg Asp His	atg gto Met Val	ctg ctg Leu Leu	gag ttc Glu Phe 185	Val Thr	gcc gcc Ala Ala	ggg atc Gly Ile 190	act 576 Thr
ctc ggc ato Leu Gly Met 195	: Asp Glu						600
<210> 47 <211> 200 <212> PRT <213> Arti	ficial.						
<220> <223> modi	fied fra	g.; YFPF2	2A with	Y66F m	utation +	Met @ ]	posit. 1
<400> 47							
Met Gly Lys	Leu Thr 5	Leu Lys	Phe Ile	Cys Thr 10	Thr Gly	Lys Leu 15	Pro
Val Pro Trp	Pro Thr 20	Leu Val	Thr Thr	Phe Gly		Leu Gln 30	Cys
Phe Ala Aro	Tyr Pro	Asp His	Met Lys 40	Arg His	Asp Phe 45	Phe Lys	Ser
Ala Met Pro	Glu Gly	Tyr Val 55	Gln Glu	Arg Thr	Ile Phe 60	Phe Lys	Asp
Asp Gly Asr	Tyr Lys				Phe Glu		
Leu Val Asr	Arg Ile 85	Glu Leu	Lys Gly	Ile Asp 90	Phe Lys	Glu Asp 95	Gly
Asn Ile Leu	Gly His	Lys Leu	Glu Tyr 105	Asn Tyr		His Asn 110	Val
Tyr Ile Met		Lys Gln	Lys Asn 120	Gly Ile	Lys Val	Asn Phe	Lys
Ile Arg His	Asn Ile	Glu Asp 135	Gly Ser	Val Gln	Leu Ala . 140	Asp His	Tyr

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 48 <211> 597 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A with Q69K mutation <220> <221> CDS <222> (1)..(597) <400> 48 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile

115		120	125
		agc gtg cag ctc gcc Ser Val Gln Leu Ala 140	
		ggc ccc gtg ctg ctg Gly Pro Val Leu Leu 155	
tac ctg agc t Tyr Leu Ser T	ac cag tcc gcc Cyr Gln Ser Ala 165	ctg agc aaa gac ccc Leu Ser Lys Asp Pro 170	aac gag aag cgc 528 Asn Glu Lys Arg 175
Asp His Met V		ttc gtg acc gcc gcc Phe Val Thr Ala Ala 185	
	gag ctg tac aag Hu Leu Tyr Lys		597
<210> 49 <211> 199 <212> PRT <213> Artifi	cial		
<220> <223> modifi	ed frag.; YFPF	2A with O69K mutat	ion
	•	DII WICH QOOK MUCUC	1011
<400> 49	2 1	zii wien goyk maeac	
	hr Leu Lys Phe 5	Ile Cys Thr Thr Gly	
Gly Lys Leu T  Pro Trp Pro T	5	Ile Cys Thr Thr Gly	Lys Leu Pro Val 15
Gly Lys Leu T  Pro Trp Pro T  2	5 Thr Leu Val Thr	Ile Cys Thr Thr Gly 10 Thr Phe Gly Tyr Gly	Lys Leu Pro Val 15 Leu Lys Cys Phe 30
Gly Lys Leu T  Pro Trp Pro T  Ala Arg Tyr P  35	5 Thr Leu Val Thr 10 Pro Asp His Met	Ile Cys Thr Thr Gly 10  Thr Phe Gly Tyr Gly 25  Lys Arg His Asp Phe	Lys Leu Pro Val 15  Leu Lys Cys Phe 30  Phe Lys Ser Ala 45
Gly Lys Leu T  Pro Trp Pro T  Ala Arg Tyr P  35  Met Pro Glu G  50	Thr Leu Val Thr	Ile Cys Thr Thr Gly 10  Thr Phe Gly Tyr Gly 25  Lys Arg His Asp Phe 40  Glu Arg Thr Ile Phe	Lys Leu Pro Val 15  Leu Lys Cys Phe 30  Phe Lys Ser Ala 45  Phe Lys Asp Asp
Gly Lys Leu T  Pro Trp Pro T  Ala Arg Tyr P  35  Met Pro Glu G  50  Gly Asn Tyr L  65	Shr Leu Val Thr To  Pro Asp His Met Sly Tyr Val Gln 55  Sys Thr Arg Ala 70	Ile Cys Thr Thr Gly 10  Thr Phe Gly Tyr Gly 25  Lys Arg His Asp Phe 40  Glu Arg Thr Ile Phe 60  Glu Val Lys Phe Glu	Lys Leu Pro Val 15  Leu Lys Cys Phe 30  Phe Lys Ser Ala 45  Phe Lys Asp Asp  Gly Asp Thr Leu 80

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190
Gly Met Asp Glu Leu Tyr Lys 195
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<223> modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1
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<pre>&lt;223&gt; modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(600)  &lt;400&gt; 50 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro</pre> 48
<pre>&lt;223&gt; modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(600)  &lt;400&gt; 50 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
<pre>&lt;223&gt; modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(600)  &lt;400&gt; 50 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
<pre>&lt;223&gt; modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(600)  &lt;400&gt; 50 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>

	85	90	)	95
			ac tac aac agc cac sn Tyr Asn Ser His 110	
		/s Asn Gl	gc atc aag gtg aac Ly Ile Lys Val Asn 125	
			g cag ctc gcc gac al Gln Leu Ala Asp 140	
			cc gtg ctg ctg ccc co Val Leu Leu Pro 155	
			gc aaa gac ccc aac er Lys Asp Pro Asn 70	
			g acc gcc gcc ggg al Thr Ala Ala Gly 190	
ctc ggc atg gac Leu Gly Met Asp 195		/S		600
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<211> 200 <212> PRT <213> Artificia <220>		with C	069K mutation + Me	t @ posit. 1
<211> 200 <212> PRT <213> Artificia <220>		with Q	069K mutation + Me	t @ posit. 1
<211> 200 <212> PRT <213> Artificial <220> <223> modified <400> 51	frag.; YFPF2A		s Thr Thr Gly Lys	-
<pre>&lt;211&gt; 200 &lt;212&gt; PRT &lt;213&gt; Artificia &lt;220&gt; &lt;223&gt; modified &lt;400&gt; 51  Met Gly Lys Leu 1</pre>	frag.; YFPF2A Thr Leu Lys Ph 5	ne Ile Cy 10	s Thr Thr Gly Lys	Leu Pro 15
<pre>&lt;211&gt; 200 &lt;212&gt; PRT &lt;213&gt; Artificia &lt;220&gt; &lt;223&gt; modified &lt;400&gt; 51  Met Gly Lys Leu 1  Val Pro Trp Pro</pre>	frag.; YFPF2A  Thr Leu Lys Ph 5  Thr Leu Val Th	ne Ile Cy 10 nr Thr Ph 25 et Lys Ar	vs Thr Thr Gly Lys	Leu Pro 15 Lys Cys
<pre>&lt;211&gt; 200 &lt;212&gt; PRT &lt;213&gt; Artificia &lt;220&gt; &lt;223&gt; modified &lt;400&gt; 51  Met Gly Lys Leu 1  Val Pro Trp Pro</pre>	frag.; YFPF2A  Thr Leu Lys Ph 5  Thr Leu Val Th  Pro Asp His Me 40	ne Ile Cy 10 nr Thr Ph 25 et Lys Ar	vs Thr Thr Gly Lys  ne Gly Tyr Gly Leu 30  rg His Asp Phe Phe	Leu Pro 15 Lys Cys Lys Ser

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
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ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe 20 25 30	96
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	144
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	192

50					55		•			60					
ggc aad Gly Asr 65															240
gtg aad Val Asr															288
atc cto															336
atc atc															384
cgc cac Arg His	Asn														432
cag aad Gln Asr 145															480
tac cto Tyr Lei	_		_		_	_	_						_	_	528
gat cac Asp His															576
ggc atg Gly Met															597
<210><211><212><213>	53 199 PRT Arti:	ficia	al												
<220> <223>	modi	fied	fraç	g.; (	citr:	ine 1	F2A	, V68	3L/ (	Q69K	muta	atio	າຣ		
<400>	53														
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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 54 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; citrine F2A , V68L/ Q69K mutations + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 54 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 15

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

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qtq ccc tqq ccc acc ctc qtq acc acc ttc qqc tac qqc ctq atq tqc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35
                            40
                                                                      192
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
                                105
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                        135
                                                                      480
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                    150
                                        155
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
ege gat cae atg gte etg etg gag tte gtg ace gee gee ggg ate act
                                                                      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180
                                185
                                                     190
                                                                      600
ctc ggc atg gac gag ctg tac aag
Leu Gly Met Asp Glu Leu Tyr Lys
        195
                            200
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       55
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       200
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       PRT
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<223> modif. frag.; citrine F2A , V68L/ Q69K mutations + Met @ posit. 1
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Pro Asp Asn 145 150 155

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 56

<211> 597

<212> DNA

<213> Artificial

<220> <223>	modi muta		_	;cit:	rine,	/Ven	ısF2/	A, V	58L/(	Q69K,	/N146	5I/M:	153T,	/V1632	Ą	
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ccc tg Pro Tr																96
gcc cg Ala Ar																144
atg cc Met Pr 50	o Glu															192
ggc aa Gly As 65																240
gtg aa Val As																288
atc ct Ile Le										_						336
atc ac Ile Th																384
cgc ca Arg Hi 13	s Asn															432
cag aa Gln As 145																480
tac ct Tyr Le																528
gat ca Asp Hi																576
ggc at Gly Me																597

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Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

## Gly Met Asp Glu Leu Tyr Lys

<210 <211 <212 <213	.> !>	58 600 DNA Arti	ficia	al	,				·								
<220 <223	>	modi: mutat							F2A	V681	٦/Q6 <u>s</u>	ek/ni	146I,	/M153	3T/V1	.63A	
<220 <221 <222	>	CDS	.(600	0)													
	ggc	58 aag Lys															48
		tgg Trp															96
		cgc Arg 35															144
gcc Ala	atg Met 50	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp		192
		aac Asn															240
		aac Asn															288
	Ile	ctg Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn			336
		acc Thr 115															384
		cac His															432
		aac Asn															480
cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	•	528

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190 600 ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 59 <211> 200 <212> PRT <213> Artificial <220> modif. frag.; citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A <223> mutations + Met @ posit. 1 <400> 59 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys 20 25 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 95 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 140 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 155

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 200 195 <210> 60 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; CFP F2A, F64L mutation <220> <221> CDS <222> (1)..(597) <400> 60 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe 20 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc . 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arq Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc lle Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

288

336

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat

. 85

130	135		140	·
cag aac acc co Gln Asn Thr Pi 145				
tac ctg agc ta Tyr Leu Ser Ty				
gat cac atg gt Asp His Met Va			Ala Ala Gly	
ggc atg gac ga Gly Met Asp Gl 195			·	597
<210> 61 <211> 199 <212> PRT <213> Artific	cial			
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Pro Trp Pro Th	,	Thr Leu Gly 25		Gln Cys Phe 30
Ala Arg Tyr Pr 35	co Asp His Met	Lys Arg His	Asp Phe Phe 1	Lys Ser Ala
Met Pro Glu Gl 50	ly Tyr Val Gln 55	Glu Arg Thr	Ile Phe Phe 1	Lys Asp Asp
Gly Asn Tyr Ly 65	ys Thr Arg Ala 70	Glu Val Lys	Phe Glu Gly 7	Asp Thr Leu 80
Val Asn Arg II	le Glu Leu Lys 85	Gly Ile Asp 90	Phe Lys Glu A	Asp Gly Asn 95
Ile Leu Gly Hi	is Lys Leu Glu )O	Tyr Asn Tyr 105		Asn Val Tyr 110
Ile Met Ala As 115	sp Lys Gln Lys	Asn Gly Ile 120	Lys Val Asn 1	Phe Lys Ile

130		Gly Ser Val 135	Gln Leu Ala 140	Asp His Tyr	Gln
Gln Asn Thr Pr 145	o Ile Gly 7 150	Asp Gly Pro	Val Leu Leu 155	Pro Asp Asn	His 160
Tyr Leu Ser Ty	r Gln Ser i 165	Ala Leu Ser	Lys Asp Pro 170	Asn Glu Lys 175	Arg
Asp His Met Va		Glu Phe Val 185	Thr Ala Ala	Gly Ile Thr 190	Leu
Gly Met Asp Gl 195	u Leu Tyr 1	Lys			
<210> 62 <211> 600 <212> DNA <213> Artific	ial				
<220> <223> modif.	frag.; CFP	F2A, F64L m	nutation + Me	et @ posit.	1
<220> <221> CDS <222> (1)(6	00)	•			
	•				
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atg ggc aag ct Met Gly Lys Le	g acc ctg a u Thr Leu l 5	Lys Phe Ile	Cys Thr Thr 10 ctg ggc tac	Gly Lys Leu 15 ggc ctg cag	Pro tgc 96
atg ggc aag ct Met Gly Lys Le 1 gtg ccc tgg cc Val Pro Trp Pr	g acc ctg au Thr Leu I 5 c acc ctc co Thr Leu I	Lys Phe Ile gtg acc acc Val Thr Thr 25 cac atg aag	Cys Thr Thr 10  ctg ggc tac Leu Gly Tyr  cgg cac gac	Gly Lys Leu 15  ggc ctg cag Gly Leu Gln 30  ttc ttc aag	Pro tgc 96 Cys tcc 144
atg ggc aag ct Met Gly Lys Le 1 gtg ccc tgg cc Val Pro Trp Pr 20 ttc gcc cgc ta Phe Ala Arg Ty	g acc ctg a u Thr Leu I 5 c acc ctc g o Thr Leu I c ccc gac o r Pro Asp I a ggc tac g u Gly Tyr I	gtg acc acc Val Thr Thr 25 cac atg aag His Met Lys 40 gtc cag gag	Cys Thr Thr 10  ctg ggc tac Leu Gly Tyr  cgg cac gac Arg His Asp  cgc acc atc	Gly Lys Leu 15  ggc ctg cag Gly Leu Gln 30  ttc ttc aag Phe Phe Lys 45  ttc ttc aag	Pro  tgc 96 Cys  tcc 144 ser  gac 192
atg ggc aag ct Met Gly Lys Le 1 gtg ccc tgg cc Val Pro Trp Pr 20 ttc gcc cgc ta Phe Ala Arg Ty 35 gcc atg ccc ga Ala Met Pro Gl	g acc ctg acc Thr Leu I 5 c acc ctc g Thr Leu I c ccc gac c r Pro Asp I a ggc tac g Gly Tyr I c aag acc c	Lys Phe Ile  gtg acc acc Val Thr Thr 25  cac atg aag His Met Lys 40  gtc cag gag Val Gln Glu 55  cgc gcc gag	Cys Thr Thr 10  ctg ggc tac Leu Gly Tyr  cgg cac gac Arg His Asp  cgc acc atc Arg Thr Ile 60  gtg aag ttc	Gly Lys Leu 15  ggc ctg cag Gly Leu Gln 30  ttc ttc aag Phe Phe Lys 45  ttc ttc aag Phe Phe Lys	pro  tgc 96 Cys  tcc 144 ser  gac 192 Asp  acc 240
atg ggc aag ct Met Gly Lys Le 1  gtg ccc tgg cc Val Pro Trp Pr 20  ttc gcc cgc ta Phe Ala Arg Ty 35  gcc atg ccc ga Ala Met Pro Gl 50  gac ggc aac ta Asp Gly Asn Ty	g acc ctg ac Thr Leu I 5 c acc ctc g Thr Leu I c ccc gac c r Pro Asp I a ggc tac g I Gly Tyr I c aag acc c Lys Thr I 70 c atc gag o	Lys Phe Ile gtg acc acc Val Thr Thr 25 cac atg aag His Met Lys 40 gtc cag gag Val Gln Glu 55 cgc gcc gag Arg Ala Glu ctg aag ggc	Cys Thr Thr 10  ctg ggc tac Leu Gly Tyr  cgg cac gac Arg His Asp  cgc acc atc Arg Thr Ile 60  gtg aag ttc Val Lys Phe 75  atc gac ttc	Gly Lys Leu 15  ggc ctg cag Gly Leu Gln 30  ttc ttc aag Phe Phe Lys 45  ttc ttc aag Phe Phe Lys Gag ggc gac Glu Gly Asp aag gag gac gac	tgc 96 Cys 96 tcc 144 ser 192 Asp 240 Thr 80 ggc 288

100 105 110

Tyr Ile Met Ala Asp Lys 115		ggc atc aag gtg Gly Ile Lys Val 125	
atc cgc cac aac atc gag Ile Arg His Asn Ile Glu 130			
cag cag aac acc ccc atc Gln Gln Asn Thr Pro Ile 145 150	Gly Asp Gly I		
cac tac ctg agc tac cag His Tyr Leu Ser Tyr Gln 165	Ser Ala Leu 8		
cgc gat cac atg gtc ctg Arg Asp His Met Val Leu 180		Val Thr Ala Ala	
ctc ggc atg gac gag ctg Leu Gly Met Asp Glu Leu 195			600
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<213> Artificial			
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	P F2A, F64L mu	utation + Met @	posit. 1
<220> <223> modif. frag.; CF	Lys Phe Ile (		-
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<220> <223> modif. frag.; CF <400> 63  Met Gly Lys Leu Thr Leu 1 5  Val Pro Trp Pro Thr Leu 20  Phe Ala Arg Tyr Pro Asp	Lys Phe Ile (  Val Thr Thr I  25  His Met Lys A	Cys Thr Thr Gly 10  Leu Gly Tyr Gly  Arg His Asp Phe 45	Lys Leu Pro 15 Leu Gln Cys 30 Phe Lys Ser
<220> <223> modif. frag.; CF <400> 63  Met Gly Lys Leu Thr Leu 1 5  Val Pro Trp Pro Thr Leu 20  Phe Ala Arg Tyr Pro Asp 35  Ala Met Pro Glu Gly Tyr	Lys Phe Ile of State	Cys Thr Thr Gly 10  Leu Gly Tyr Gly  Arg His Asp Phe 45  Arg Thr Ile Phe 60	Lys Leu Pro 15  Leu Gln Cys 30  Phe Lys Ser  Phe Lys Asp

100	eu Glu Tyr Asn 105	Tyr Asn Ser His 110	Asn Val
Tyr Ile Met Ala Asp Lys G	n Lys Asn Gly	Ile Lys Val Asn 125	Phe Lys
Ile Arg His Asn Ile Glu As		Gln Leu Ala Asp 140	His Tyr
Gln Gln Asn Thr Pro Ile G 145 150	y Asp Gly Pro	Val Leu Leu Pro 155	Asp Asn 160
His Tyr Leu Ser Tyr Gln Se	er Ala Leu Ser 170	Lys Asp Pro Asn	Glu Lys 175
Arg Asp His Met Val Leu Le	eu Glu Phe Val 185	Thr Ala Ala Gly 190	Ile Thr
Leu Gly Met Asp Glu Leu Ty 195	r Lys 200		
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<212> DNA <213> Artificial <220>	<sup>7</sup> 2 <b>A</b> , Y66W mut	ation	
<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP I  &lt;220&gt; &lt;221&gt; CDS</pre>	c atc tgc acc	acc ggc aag ctg	
<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 64    ggc aag ctg acc ctg aag tt    Gly Lys Leu Thr Leu Lys Ph</pre>	c atc tgc acc e Ile Cys Thr 10	acc ggc aag ctg Thr Gly Lys Leu tgg ggc ctg cag	Pro Val 15 tgc ttc 96
<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 64  ggc aag ctg acc ctg aag tt Gly Lys Leu Thr Leu Lys Ph 1 5  ccc tgg ccc acc ctc gtg acc Pro Trp Pro Thr Leu Val Th</pre>	ac atc tgc acc le Ile Cys Thr 10 cc acc ttc ggc ar Thr Phe Gly 25	acc ggc aag ctg Thr Gly Lys Leu  tgg ggc ctg cag Trp Gly Leu Gln 30 gac ttc ttc aag	Pro Val 15 tgc ttc 96 Cys Phe tcc gcc 144
<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 64 ggc aag ctg acc ctg aag tt Gly Lys Leu Thr Leu Lys Ph 1 5  ccc tgg ccc acc ctc gtg ac Pro Trp Pro Thr Leu Val Th 20  gcc cgc tac ccc gac cac at Ala Arg Tyr Pro Asp His Me</pre>	ac atc tgc acc le Ile Cys Thr 10 cc acc ttc ggc r Thr Phe Gly 25 cc Lys Arg His 40 cg gag cgc acc n Glu Arg Thr	acc ggc aag ctg Thr Gly Lys Leu  tgg ggc ctg cag Trp Gly Leu Gln 30  gac ttc ttc aag Asp Phe Phe Lys 45  atc ttc ttc aag	Pro Val 15  tgc ttc 96 Cys Phe  tcc gcc 144 Ser Ala  gac gac 192

65	70	75	80
gtg aac cgc atc gag Val Asn Arg Ile Glu 85		p Phe Lys Glu Asp	
atc ctg ggg cac aag Ile Leu Gly His Lys 100			
atc atg gcc gac aag Ile Met Ala Asp Lys 115	cag aag aac ggc at Gln Lys Asn Gly Il 120	c aag gtg aac ttc a e Lys Val Asn Phe 1 125	aag atc 384 Lys Ile
cgc cac aac atc gag Arg His Asn Ile Glu 130			
cag aac acc ccc atc Gln Asn Thr Pro Ile 145			
tac ctg agc tac cag Tyr Leu Ser Tyr Gln 165		s Asp Pro Asn Glu :	
gat cac atg gtc ctg Asp His Met Val Leu 180			
ggc atg gac gag ctg Gly Met Asp Glu Leu 195	•		597
<210> 65 <211> 199 <212> PRT <213> Artificial			
<220> <223> modif. frag.;	: CFP F2A , Y66W m	utation	
<400> 65			
Gly Lys Leu Thr Leu 1 5	Lys Phe Ile Cys Th	= =	Pro Val 15
Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Gl 25	y Trp Gly Leu Gln ( 30	Cys Phe
Ala Arg Tyr Pro Asp 35	His Met Lys Arg Hi 40	s Asp Phe Phe Lys & 45	Ser Ala
Met Pro Glu Gly Tyr	Val Gln Glu Arc Th	a Ila Dha Dha I	Nan Nan

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 . 125 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 170 165 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190 Gly Met Asp Glu Leu Tyr Lys 195 <210> 66 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A , Y66W mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 66 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys 20 tto goo ego tac eco gac cac atg aag egg cac gac tto tto aag tec 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser

	35			40	٠				45				
gcc atg Ala Met 50	ccc gaa Pro Glu	ggc tac Gly Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp	192
		aag acc Lys Thr 70											240
		atc gag Ile Glu 85											288
		cac aag His Lys											336
		gac aag Asp Lys											384
		atc gag Ile Glu											432
cag cag Gln Gln 145	aac acc Asn Thr	ccc atc Pro Ile 150	ggc	gac Asp	ggc Gly	ccc Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480
		tac cag Tyr Gln 165											528
		gtc ctg Val Leu											576
		gag ctg Glu Leu		_									600
<211> 2 <212> 1	57 200 PRT Artifici	al											
<220> <223> r	nodif. f	rag.; CF	P F2	A , S	766W	mut	atio	on +	Met	@ pc	osit.	. 1	
<400>	57		•	,									
Met Gly 1	Lys Leu	Thr Leu 5	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 68 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A , S65A mutation <220> <221> CDS

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<400> 68

1	5	10		15	
			tac ggc ctg ca Tyr Gly Leu Gl 30	n Cys Phe	96
	Asp His Met I		gac ttc ttc aa Asp Phe Phe Ly 45		144
			atc ttc ttc aa Ile Phe Phe Ly 60		192
			g ttc gag ggc ga s Phe Glu Gly As 75		240
			ttc aag gag ga Phe Lys Glu As		288
	s Lys Leu Glu :		aac agc cac aa Asn Ser His As 11	n Val Tyr	336
	D Lys Gln Lys A		aag gtg aac tt Lys Val Asn Ph 125		384
			g ctc gcc gac ca Leu Ala Asp Hi 140		432
			ctg ctg ccc ga Leu Leu Pro As 155		480
			gac ccc aac ga Asp Pro Asn Gl		528
	Leu Leu Glu I		gcc gcc ggg at Ala Ala Gly Il	e Thr Leu	576
ggc atg gac gac Gly Met Asp Glo 195					597
<210> 69 <211> 199 <212> PRT <213> Artific	lal				
<220> <223> modif. :	frag.; CFP F2A	, S65A mu	tation		

<400> 69

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 70

<211> 600

<212> DNA

<213> Artificial

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<22 <22 <22	1> (	CDS	.(60	0)												
	ggc				ctg Leu											48
					ctc Leu											96
ttc Phe	gcc Ala	cgc Arg 35	tac Tyr	ccc Pro	gac Asp	cac His	atg Met 40	aag Lys	cgg Arg	cac His	gac Asp	ttc Phe 45	ttc Phe	aag Lys	tcc Ser	144
					tac Tyr											192
					acc Thr 70											240
					gag Glu											288
					aag Lys											336
					aag Lys											384
					gag Glu											432
					atc Ile 150											480
					cag Gln											528
					ctg Leu											576
					ctg Leu											600

<210> 71

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2A , S65A mutation + Met @ posit 1

<400> 71

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys

<210 <211 <212 <213	L> 2>	72 597 DNA Arti:	ficia	al												
<220 <223		modi:	f. f	rag.	; CGI	FP F2	2 <b>A</b> , 8	S65A,	/Y66I	W/T2	03Y	muta	atio	າຣ		
<220 <220 <220	l >	CDS (1).	. (59	7)												
	aag	72 ctg Leu													4	4 8
		ccc Pro													<u> </u>	96
		tac Tyr 35													14	14
		gaa Glu													. 19	€
		tac Tyr													24	1 C
		cgc Arg													28	38
		ggg Gly													33	36
		gcc Ala 115													38	34
		aac Asn													43	32
		acc Thr													4 8	30
		agc Ser													52	28

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 597 ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195 <210> 73 <211> 199 <212> PRT <213> Artificial <220> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations <223> <400> 73 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe 25 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210 <211 <212 <213	L> ( 2> 1	74 500 ONA Artii	ficia	al													
<220 <223		modi	E. fi	rag.	; CGI	FP F2	2A, S	565A,	/Y66W	V/T20	) 3Υ τ	nutai	cions	1 + E	Met @	pos.	1
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	ggc	74 aag Lys															48
		tgg Trp													tgc Cys		96
	_	cgc Arg 35			_		_	_			_			_			144
		ccc Pro															192
		aac Asn															240
		aac Asn															288
		ctg Leu															336
		atg Met 115															384
		cac His															432

130	135		140	
			gtg ctg ctg ccc Val Leu Leu Pro 155	
			aaa gac ccc aac Lys Asp Pro Asn	
			acc gcc gcc ggg Thr Ala Ala Gly 190	
ctc ggc atg gac Leu Gly Met Asp 195				600
<210> 75 <211> 200 <212> PRT <213> Artificia	al			
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<400> 75				
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Val Pro Trp Pro 20	Thr Leu Val	Thr Thr Phe 25	Ala Trp Gly Leu 30	Gln Cys
Phe Ala Arg Tyr 35	Pro Asp His	Met Lys Arg 40	His Asp Phe Phe 45	Lys Ser
Ala Met Pro Glu 50	Gly Tyr Val 55	Gln Glu Arg	Thr Ile Phe Phe	Lys Asp
Asp Gly Asn Tyr 65	Lys Thr Arg 70	Ala Glu Val	Lys Phe Glu Gly 75	Asp Thr 80
Leu Val Asn Arg	Ile Glu Leu 85	Lys Gly Ile 90	Asp Phe Lys Glu	Asp Gly 95
Asn Ile Leu Gly 100	His Lys Leu	Glu Tyr Asn 105	Tyr Asn Ser His	Asn Val
Tyr Ile Met Ala 115	Asp Lys Gln	Lys Asn Gly	Ile Lys Val Asn 125	Phe Lys

130	e Glu Asp Gly 135	Ser Val Gln Le	eu Ala Asp His 40	Tyr
Gln Gln Asn Thr Pr 145	o Ile Gly Asp	Gly Pro Val Le	eu Leu Pro Asp	Asn 160
His Tyr Leu Ser Ty		Leu Ser Lys As	sp Pro Asn Glu 175	Lys
Arg Asp His Met Va	l Leu Leu Glu	Phe Val Thr Al 185	la Ala Gly Ile 190	Thr
Leu Gly Met Asp Gl 195	u Leu Tyr Lys 200			
<210> 76 <211> 597 <212> DNA <213> Artificial				
<220> <223> modif. frag	. CGFP F2A ,	F64L/S65T/Y66W/	/M153T/V163A/T2	203Y
	•			
<220> <221> CDS <222> (1)(597)				
<221> CDS				
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<221> CDS <222> (1)(597)  <400> 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1 5  ccc tgg ccc acc ct Pro Trp Pro Thr Le	u Lys Phe Ile c gtg acc acc u Val Thr Thr c cac atg aag	Cys Thr Thr Gl 10  ctg acc tgg gg Leu Thr Trp Gl 25  cgg cac gac tt	ly Lys Leu Pro 15 gc ctg cag tgc ly Leu Gln Cys 30 tc ttc aag tcc	val ttc 96 Phe gcc 144
<pre>&lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1</pre>	u Lys Phe Ile c gtg acc acc u Val Thr Thr c cac atg aag p His Met Lys 40 c gtc cag gag	Cys Thr Thr Gl 10  ctg acc tgg gg Leu Thr Trp Gl 25  cgg cac gac tt Arg His Asp Ph  cgc acc atc tt	Lys Leu Pro 15  gc ctg cag tgc ly Leu Gln Cys 30  tc ttc aag tcc he Phe Lys Ser 45  tc ttc aag gac he Phe Lys Asp	Val ttc 96 Phe gcc 144 Ala gac 192
<pre>&lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1</pre>	u Lys Phe Ile c gtg acc acc u Val Thr Thr c cac atg aag p His Met Lys 40 c gtc cag gag r Val Gln Glu 55 c cgc gcc gag	Cys Thr Thr Gl 10  ctg acc tgg gg Leu Thr Trp Gl 25  cgg cac gac tt Arg His Asp Ph  cgc acc atc tt Arg Thr Ile Ph 60  gtg aag ttc ga	Lys Leu Pro 15  gc ctg cag tgc ly Leu Gln Cys 30  tc ttc aag tcc he Phe Lys Ser 45  tc ttc aag gac he Phe Lys Asp 0  ag ggc gac acc lu Gly Asp Thr	Val ttc 96 Phe gcc 144 Ala gac 192 Asp ctg 240

atc ctg ggg Ile Leu Gly				n Tyr A		His .				336
atc acc gcc Ile Thr Ala 115										384
cgc cac aac Arg His Asn 130			Ser Va							432
cag aac acc Gln Asn Thr 145				o Val I						480
tac ctg agc Tyr Leu Ser		Ser Ala					Glu			528
gat cac atg Asp His Met				l Thr A		Gly				576
ggc atg gac Gly Met Asp 195	-	_								597
<210> 77 <211> 199 <212> PRT <213> Arti	ficial									
	f. frag. tions	CGFP F2	A , F64	L/S65T/	/Y66W/M1	L53T/	V163	A/T2	203Y	
<400> 77										
Gly Lys Leu 1	Thr Leu 5	_	Ile Cy		_	Lys :		Pro 15	Val	
Pro Trp Pro	Thr Leu 20	Val Thr	Thr Le	ı Thr I	Irp Gly		Gln 30	Cys	Phe	
Ala Arg Tyr 35	Pro Asp	His Met	Lys Arg	g His A	Asp Phe	Phe 3	Lys	Ser	Ala	
Met Pro Glu										
50	Gly Tyr	Val Gln 55	Glu Ar	g Thr I	Ile Phe 60	Phe :	Lys	Asp	Asp	

Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile	Thr	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	·
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
<210 <211 <212 <213	L> 6 2> I	78 500 ONA Artif	Ficia	al												
<220 <223	3> r	modif mutat		_					365T/	<sup>/</sup> Y66V	V/M15	53T/V	/1,63/	A/T2(	)3Y	
<220 <221 <222	L> (	CDS (1)	. (600	))												
<400 atg Met 1	ggc	78 aag Lys	ctg Leu	acc Thr 5	ctg Leu	aag Lys	ttc Phe	atc Ile	tgc Cys 10	acc Thr	acc Thr	ggc Gly	aag Lys	ctg Leu 15	ccc Pro	4 8
gtg Val	ccc Pro	tgg Trp	ccc Pro 20	acc Thr	ctc Leu	gtg Val	acc Thr	acc Thr 25	ctg Leu	acc Thr	tgg Trp	ggc Gly	ctg Leu 30	cag Gln	tgc Cys	96
		cgc Arg														144

gcc atg ccc Ala Met Pro 50						
gac ggc aac Asp Gly Asn 65	Tyr Lys T					
ctg gtg aac Leu Val Asn						
aac atc ctg Asn Ile Leu						
tat atc acc Tyr Ile Thr 115			s Asn Gly		a Asn Phe	
atc cgc cac Ile Arg His 130						
cag cag aac Gln Gln Asn 145	Thr Pro I					
cac tac ctg His Tyr Leu				Lys Asp Pr		Lys
cgc gat cac Arg Asp His						
ctc ggc atg Leu Gly Met 195		_	S			600
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	. –	CGFP F2A, et @ posit		/Y66W/M153T	/V163A/T2	03Y
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Met Gly Lys	Leu Thr L 5	Leu Lys Ph	e Ile Cys 10	Thr Thr Gl	y Lys Leu 15	Pro
Val Pro Trp	Pro Thr L	Leu Val Th	r Thr Leu 25	Thr Trp Gl	y Leu Gln 30	Cys

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 80

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modif. frag., CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A mutations

<220>

<221> CDS

<222> (1)..(597)

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				gtg Val						96
				cac His						144
				gtc Val						192
				cgc Arg 70						240
				ctg Leu						288
				ctg Leu						336
				cag Gln						384
				gac Asp						432
				ggc Gly 150						480
				tcc Ser						528
				ctg Leu						576
				tac Tyr						597

<210> 81

<211> 199

<212> PRT <213> Artificial

<220>

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mutations

<400> 81

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1  $\phantom{0}$  5  $\phantom{0}$  10  $\phantom{0}$  15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 82 <211> 600

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<220> <223>	modi muta	f.f: tion	_		-	55 <b>T</b> /	Y66W,	/N140	5I/M:	153T,	/V16:	3 <b>A</b>	
<220> <221> <222>		.(60	0)										
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gtg co Val Pr													96
ttc go Phe Al													144
gcc at Ala Me 50	t Pro												192
gac gg Asp Gl 65													240
ctg gt Leu Va													288
aac at Asn Il													336
tat at Tyr Il		Ala											384
atc co Ile Ar 13	g His												432
cag ca Gln Gl 145													480
cac ta His Ty													528
cgc ga Arg As													576

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 83

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag. CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A
 mutations + Met @ posit. 1

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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 84 <211> 597 <212> DNA <213> Artificial <220> modif. frag. CFP F2A, N146I mutation <223> <220> <221> CDS <222> (1)..(597) <400> 84 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ecc tgg ecc acc etc gtg acc acc tte gge tac gge etg eag tge tte 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 95 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

185

180

145

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195	597
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<220> <223> modif. frag. CFP F2A, N146I mutation	
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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 155 160	

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 86 <211> 600 <212> DNA <213> Artificial <220> modif. frag. CFP F2A, N146I mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 86 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag gac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140
cag cag aac acc ccc atc Gln Gln Asn Thr Pro Ile 145	e Gly Asp Gly Pro Val	
cac tac ctg agc acc cag His Tyr Leu Ser Thr Glr 165		
cgc gat cac atg gtc ctg Arg Asp His Met Val Let 180		
ctc ggc atg gac gag ctg Leu Gly Met Asp Glu Leu 195		600
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Val Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Gly 25	Tyr Gly Leu Gln Cys
Phe Ala Arg Tyr Pro Asp 35	His Met Lys Arg His	Asp Phe Phe Lys Ser
Ala Met Pro Glu Gly Tyr 50	Val Gln Glu Arg Thr 55	Ile Phe Phe Lys Asp 60
Asp Gly Asn Tyr Lys Thr	Arg Ala Glu Val Lys 75	Phe Glu Gly Asp Thr 80
Leu Val Asn Arg Ile Glu 85	Leu Lys Gly Ile Asp 90	Phe Lys Glu Asp Gly 95
Asn Ile Leu Gly His Lys 100	Leu Glu Tyr Asn Tyr 105	Ile Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

130	Asn Ile Gl	u Asp Gl	y Ser Val	Gln Leu 140	Ala Asp	His	Tyr
Gln Gln Asn T	Thr Pro II		p Gly Pro	Val Leu 155	Leu Pro	_	Asn 160
His Tyr Leu S	Ser Thr Gl	n Ser Ala	a Leu Ser 170		Pro Asn	Glu 175	Lys
Arg Asp His M	Met Val Le 180	u Leu Gl	u Phe Val 185	Thr Ala	Ala Gly 190	Ile	Thr
Leu Gly Met A	Asp Glu Le	u Tyr Ly: 20					
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<220>							
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	acc ctg aa						
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<222> (1)( <400> 88 ggc aag ctg a Gly Lys Leu T 1  ccc tgg ccc a Pro Trp Pro T 2 gcc cgc tac c Ala Arg Tyr F	acc ctg aa Thr Leu Ly 5 acc ctc gt Thr Leu Va 20 acc gac ca Pro Asp Hi	g acc acc l Thr The c atg aag s Met Ly 40 c cag gag	e Cys Thr 10 c ttc ggc r Phe Gly 25 c cgg cac s Arg His	Thr Gly tac ggc Tyr Gly gac ttc Asp Phe atc ttc	Lys Leu  ctg cag Leu Gln 30  ttc aag Phe Lys 45  ttc aag	Pro 15 tgc Cys tcc cys	ttc 96 Phe gcc 144 Ala gac 192
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<pre>&lt;222&gt; (1)( &lt;400&gt; 88 ggc aag ctg a Gly Lys Leu T 1  ccc tgg ccc a Pro Trp Pro T  gcc cgc tac c Ala Arg Tyr P</pre>	acc ctg aa Thr Leu Ly 5 acc ctc gt Thr Leu Va 20 acc gac ca Pro Asp Hi agc tac gt Gly Tyr Va aag acc cg Lys Thr Ar 70 atc gag ct	g acc acc l Thr Th: c atg aag s Met Ly: 40 c cag gag l Gln Gli 55 c gcc gag g Ala Gli g aag gg	c ttc ggc r Phe Gly 25 g cgg cac s Arg His g cgc acc l Arg Thr g gtg aag l Val Lys c atc gac	Thr Gly tac ggc Tyr Gly gac ttc Asp Phe atc ttc Ile Phe 60 ttc gag Phe Glu 75 ttc aag	Lys Leu  ctg cag Leu Gln 30  ttc aag Phe Lys 45  ttc aag Phe Lys  ggc gac Gly Asp  gag gac	Pro 15 tgc Cys tcc Ser 2 gac Asp 2 acc Thr 1	Val  ttc 96 Phe  gcc 144 Ala  gac 192 Asp  ctg 240 Leu 80 aac 288

100 105 110

iie iii	gcc Ala 115														384
cgc cac Arg His	Asn	atc Ile	gag Glu	gac Asp	ggc Gly 135	agc Ser	gtg Val	cag Gln	ctc Leu	gcc Ala 140	gac Asp	cac His	tac Tyr	cag Gln	432
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tac ctg Tyr Leu															528
gat cac Asp His															576
ggc atg Gly Met	_		_		_										597
<212>	89 199 PRT Artii	Eicia	al												
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Ile Leu Gly	His Lys 100	Leu Glu	Tyr Asn 105	Tyr Asn	Ser His	Asn Val 110	Tyr
Ile Thr Ala 115	Asp Lys	_	Asn Gly 120	Ile Lys	Val Asn 125	Phe Lys	Ile
Arg His Asn 130	Ile Glu	Asp Gly 135	Ser Val	Gln Leu	Ala Asp 140	His Tyr	Gln
Gln Asn Thr 145	Pro Ile	Gly Asp 150	Gly Pro	Val Leu 155	Leu Pro	Asp Asn	His 160
Tyr Leu Ser	Thr Gln 165	Ser Ala	Leu Ser	Lys Asp 170	Pro Asn	Glu Lys 175	Arg
Asp His Met	Val Leu 180	Leu Glu	Phe Val 185	Thr Ala	Ala Gly	Ile Thr 190	Leu
Gly Met Asp 195	Glu Leu	Tyr Lys					
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ttc gcc cgc Phe Ala Arg 35		Asp His					
gcc atg ccc							

			aag ttc gag ggc Lys Phe Glu Gly 75	
			gac ttc aag gag Asp Phe Lys Glu	
			tac aac agc cac Tyr Asn Ser His 110	
			atc aag gtg aac Ile Lys Val Asn 125	
			cag ctc gcc gac Gln Leu Ala Asp 140	
			gtg ctg ctg ccc Val Leu Leu Pro 155	
	_		aaa gac ccc aac Lys Asp Pro Asn	
			acc gcc gcc ggg Thr Ala Ala Gly 190	
ctc ggc atg gac Leu Gly Met Asp 195		-		600
<210> 91 <211> 200 <212> PRT <213> Artificia	al			
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Val Pro Trp Pro	Thr Leu Val	Thr Thr Phe 25	Gly Tyr Gly Leu 30	Gln Cys
Phe Ala Arg Tyr 35	Pro Asp His	Met Lys Arg 40	His Asp Phe Phe 45	Lys Ser

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 92 <211> 597 <212> DNA <213> Artificial <223> modif. frag. CFP F2A, N146I/ M153T mutations <220> <221> CDS <222> (1)..(597) <400> 92 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

			20					25					30		
											ttc Phe				144
											ttc Phe 60				192
											gag Glu				240
		_			_	_			_		aag Lys		_		288
											agc Ser				336
											gtg Val				384
											gcc Ala 140				432
											ctg Leu				480
											ccc Pro				528
											gcc Ala				576
	atg Met														597
<210 <211 <212 <213	L> 1 2> E	93 199 PRT Artif	ficia	al											
<220 <223		nodif	Ē. fi	rag.	CFP	F2A,	N14	161/	M153	3T mi	ıtati	ons			

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 55 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 94 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1 <220> <221> CDS

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	0 >															
atg Met 1	ggc Gly	aag Lys	ctg Leu	acc Thr 5	ctg Leu	aag Lys	ttc Phe	atc Ile	tgc Cys 10	acc Thr	acc Thr	ggc Gly	aag Lys	ctg Leu 15	ccc Pro	48
gtg Val	ccc Pro	tgg Trp	ccc Pro 20	acc Thr	ctc Leu	gtg Val	acc Thr	acc Thr 25	ttc Phe	ggc Gly	tac Tyr	ggc Gly	ctg Leu 30	cag Gln	tgc Cys	96
ttc Phe	gcc Ala	cgc Arg 35	tac Tyr	ccc Pro	gac Asp	cac His	atg Met 40	aag Lys	cgg Arg	cac His	gac Asp	ttc Phe 45	ttc Phe	aag Lys	tcc Ser	144
gcc Ala	atg Met 50	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp	192
gac Asp 65	ggc Gly	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
ctg Leu	gtg Val	aac Asn	cgc Arg	atc Ile 85	gag Glu	ctg Leu	aag Lys	ggc Gly	atc Ile 90	gac Asp	ttc Phe	aag Lys	gag Glu	gac Asp 95	ggc Gly	288
aac Asn	atc Ile	ctg Leu	999 Gly 100	cac His	aag Lys	ctg Leu	gag Glu	tac Tyr 105	aac Asn	tac Tyr	atc Ile	agc Ser	cac His 110	aac Asn	gtc Val	336
tat Tyr	atc Ile	acc Thr 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gtg Val 125	aac Asn	ttc Phe	aag Lys	384
atc Ile	cgc Arg 130	cac His	aac Asn	atc Ile	gag Glu	gac Asp 135	ggc Gly	agc Ser	gtg Val	cag Gln	ctc Leu 140	gcc Ala	gac Asp	cac His	tac Tyr	432
cag Gln 145	cag Gln	aac Asn	acc Thr	ccc Pro	atc Ile 150	ggc Gly	gac Asp	ggc Gly	ccc Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480
cac His	tac Tyr	ctg Leu	agc Ser	acc Thr 165	cag Gln	tcc Ser	gcc Ala	ctg Leu	agc Ser 170	aaa Lys	gac Asp	ccc Pro	aac Asn	gag Glu 175	aag Lys	528
cgc Arg	gat Asp	cac His	atg Met 180	gtc Val	ctg Leu	ctg Leu	gag Glu	ttc Phe 185	gtg Val	acc Thr	gcc Ala	gcc Ala	999 Gly 190	atc Ile	act Thr	576
			gac Asp													600

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<220>

<223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1  $\,$ 

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys

195 200

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		ccc Pro														96
		tac Tyr 35														144
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ggc Gly 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240
		cgc Arg														288
		ggg Gly		Lys			Tyr		Tyr							336
atc Ile	acc Thr	gcc Ala 115	gac Asp	aag Lys	cag Gln	aag Lys	aac Asn 120	ggc Gly	atc Ile	aag Lys	gtg Val	aac Asn 125	ttc Phe	aag Lys	atc Ile	384
		aac Asn														432
		acc Thr														480
		agc Ser														528

165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

576

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<213> Artificial

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Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 98 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T mutations + Met @ posit. 1 <220> <221> CDS <222> (1) .. (600) <400> 98 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 tat atc acc gcc gac aag cag aag ggc atc aag gtg aac ttc aag 384 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

			aac Asn													432
			acc Thr													480
			agc Ser													528
			atg Met 180													576
			gac Asp									•				600
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<220 <223	3> r		E. fi	-					565T,	/Y66W	N/N14	16I/N	41537	Г		٠
<400	)> 9	99									,					
Met 1	Gly	Lys	Leu	Thr 5	Leu	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val	Pro	Trp	Pro 20	Thr	Leu	Val	Thr	Thr 25	Leu	Thr	Trp	Gly	Leu 30	Gln	Cys	
Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala	Met 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	.Asp	
Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu	Val	Asn	Ara	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	
			J	85					90	٠.				95		

Tyr	Ile	Thr 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Thr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Įle	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
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											ggc Gly					96
											ttc Phe					144
											ttc Phe 60					192
ggc Gly 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240

gtg aac cgc Val Asn Arg								288
atc ctg ggg Ile Leu Gly								336
atc atg gcc Ile Met Ala 115								384
cgc cac aac Arg His Asn 130								432
cag aac acc Gln Asn Thr 145								480
tac ctg agc Tyr Leu Ser							arg	528
gat cac atg Asp His Met								576
ggc atg gac Gly Met Asp 195		_						597
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Pro Trp Pro	Thr Leu 20	Val Thr	Thr Phe 25	Gly Tyr	Gly Leu	Gln Cys	Phe	
Ala Arg Tyr 35	Pro Asp	His Met	Lys Arg 40	His Asp	Phe Phe 45	Lys Ser	Ala	
Met Pro Glu 50	Gly Tyr	Val Gln 55	Glu Arg	Thr Ile	Phe Phe	Lys Asp	Asp	

Gly 65	Asn	Tyr	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile	Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Thr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
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	ggc			acc Thr 5												48
				acc Thr												96
				ccc Pro												144

3	35			40					45				
gcc atg o Ala Met I 50													192
gac ggc a Asp Gly A 65													240
ctg gtg a Leu Val A	Asn Arg												288
aac atc d Asn Ile I													336
tat atc a Tyr Ile M													384
atc cgc o Ile Arg H 130													432
cag cag a Gln Gln A 145													480
cac tac d His Tyr I	Leu Ser												528
cgc gat c Arg Asp H													576
ctc ggc a Leu Gly M													600
<210> 10 <211> 20 <212> PF <213> Ar	00	1											·
	odif. fr	ag.; CFF	F2A	., V1	.63A	muta	ition	1 + M	iet @	) pos	sit.	1	
<400> 10													
Met Gly I 1		Thr Leu 5	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

Phe Ala Arq Tyr Pro Asp His Met Lys Arq His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 190 Leu Gly Met Asp Glu Leu Tyr Lys <210> 104 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A, N146I/ V163A mutations <220> <221> CDS

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		cag gag cgc Gln Glu Arg 55			
		gcc gag gtg Ala Glu Val			
		aag ggc atc Lys Gly Ile			
		gag tac aac Glu Tyr Asn 105			
	a Asp Lys Gln	aag aac ggc Lys Asn Gly 120			
		ggc agc gtg Gly Ser Val 135			
		gac ggc ccc Asp Gly Pro			
		gcc ctg agc Ala Leu Ser			Arg
		gag ttc gtg Glu Phe Val 185			
	gag ctg tac o Glu Leu Tyr	•			597

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<220>

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Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys

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       DNA
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       CDS
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Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                25
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50
                        55
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
                                                         95
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag
                                                                      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115
ato ogo cao aac ato gag gao ggo ago gtg cag oto goo gao cao tao
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145
                                         155
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
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cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 ctc ggc atg gac gag ctg tac aag 600 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 107 <211> 200 <212> PRT <213> Artificial <220> <223> modif. frag.; CFP F2A, N146I/V163A mutations + Met @ posit. 1 <400> 107 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 5 10 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn

155

150

145

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 108 <211> 597 <212> DNA <213> Artificial <220> <223> modif. fraq.; CFP F2A, M153T/V163A mutations <220> <221> CDS <222> (1)..(597) <400> 108 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ecc tgg ecc acc etc gtg acc acc tte gge tac gge etg eag tge tte Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 qqc aac tac aaq acc cqc qcc qaq qtq aaq ttc qaq qqc qac acc ctq 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120

432

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

130	135		140		
cag aac acc ccc Gln Asn Thr Pro 145					480
tac ctg agc acc Tyr Leu Ser Thr		Leu Ser L			528
gat cac atg gtc Asp His Met Val 180	Leu Leu Glu				576
ggc atg gac gag Gly Met Asp Glu 195					597
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<220> <223> modif. f	rag.; CFP F2	A, M153T/V	163A mutations		
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Pro Trp Pro Thr 20	Leu Val Thr	Thr Phe G 25	ly Tyr Gly Leu	Gln Cys Phe 30	
Ala Arg Tyr Pro 35	Asp His Met	Lys Arg H 40	is Asp Phe Phe 45	Lys Ser Ala	
Met Pro Glu Gly 50	Tyr Val Gln 55	Glu Arg T	hr Ile Phe Phe 60	Lys Asp Asp	
Gly Asn Tyr Lys	Thr Arg Ala	Glu Val L	ys Phe Glu Gly 75.	Asp Thr Leu 80	
Val Asn Arg Ile	Glu Leu Lys 85		sp Phe Lys Glu 0	Asp Gly Asn 95	
Ile Leu Gly His	Lys Leu Glu	Tyr Asn T	yr Asn Ser His	Asn Val Tyr 110	
Ile Thr Ala Asp	Lys Gln Lys	Asn Gly I 120	le Lys Ala Asn 125	Phe Lys Ile	

Arg His Asn Ile 130		Gly Ser Val 135	Gln Leu Ala		Tyr Gln	
Gln Asn Thr Pro 145	Ile Gly A	Asp Gly Pro	Val Leu Leu 155	Pro Asp	Asn His 160	
Tyr Leu Ser Thr	Gln Ser A	Ala Leu Ser	Lys Asp Pro	Asn Glu	Lys Arg 175	
Asp His Met Val	Leu Leu G	Glu Phe Val 185	Thr Ala Ala	Gly Ile 190	Thr Leu	
Gly Met Asp Glu 195	Leu Tyr I	Lys	·			
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<pre>&lt;221&gt; CDS &lt;222&gt; (1)(600 &lt;400&gt; 110 atg ggc aag ctg Met Gly Lys Leu 1  gtg ccc tgg ccc Val Pro Trp Pro</pre>	acc ctg a Thr Leu I  5  acc ctc g Thr Leu V  ccc gac c Pro Asp H  ggc tac g Gly Tyr V  aag acc c Lys Thr A 70  atc gag c	Lys Phe Ile  gtg acc acc Val Thr Thr 25  cac atg aag His Met Lys 40  gtc cag gag Val Gln Glu 55  cgc gcc gag Arg Ala Glu  ctg aag ggc	Cys Thr Thrillo  ttc ggc tac Phe Gly Tyr  cgg cac gac Arg His Asp  cgc acc atc Arg Thr Ile 60  gtg aag ttc Val Lys Phe 75  atc gac ttc	ggc ctg Gly Leu 30 ttc ttc Phe Phe 45 ttc ttc Phe Phe Ggag ggc Glu Gly aag gag	Leu Pro 15  cag tgc Gln Cys  aag tcc Lys Ser  aag gac Lys Asp  gac acc Asp Thr 80  gac ggc 28	96

	100		105	:	110	
tat atc acc Tyr Ile Thr 115						
atc cgc cac Ile Arg His 130						
cag cag aac Gln Gln Asn 145		Gly Asp		l Leu Leu B	Pro Asp .	
cac tac ctg His Tyr Leu						
cgc gat cac Arg Asp His				r Ala Ala (		
ctc ggc atg Leu Gly Met 195						600
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Val Pro Trp	Pro Thr Leu 20	Val Thr	Thr Phe Gl 25	_	Leu Gln 30	Cys
Phe Ala Arg 35	Tyr Pro Asp	His Met	Lys Arg Hi	-	Phe Lys	Ser
		10		45		
Ala Met Pro	Glu Gly Tyr	-	Glu Arg Th		Phe Lys .	Aap
		Val Gln 55		r Ile Phe I 60	Gly Asp '	

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 100 105	Tyr Asn Ser His Asn Val 110
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	lle Lys Ala Asn Phe Lys 125
Ile Arg His Asn Ile Glu Asp Gly Ser Val 130 135	Gln Leu Ala Asp His Tyr 140
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 145 150	Val Leu Leu Pro Asp Asn 155 160
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 165 170	
Arg Asp His Met Val Leu Leu Glu Phe Val 180 185	Thr Ala Ala Gly Ile Thr 190
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
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ccc tgg ccc acc ctc gtg acc acc ttc ggc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly 20 25	
gcc cgc tac ccc gac cac atg aag cgg cac Ala Arg Tyr Pro Asp His Met Lys Arg His 35 40	
atg ccc gaa ggc tac gtc cag gag cgc acc Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 50 55	
ggc aac tac aag acc cgc gcc gag gtg aag Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys	

65	70	75		80
gtg aac cgc atc gag Val Asn Arg Ile Glu 85				
atc ctg ggg cac aag Ile Leu Gly His Lys 100	Leu Glu Tyr			
atc acc gcc gac aag Ile Thr Ala Asp Lys 115				
cgc cac aac atc gag Arg His Asn Ile Glu 130		Val Gln Leu 2		
cag aac acc ccc atc Gln Asn Thr Pro Ile 145				
tac ctg agc acc cag Tyr Leu Ser Thr Gln 165			0	_
gat cac atg gtc ctg Asp His Met Val Leu 180	Leu Glu Phe			
ggc atg gac gag ctg Gly Met Asp Glu Leu 195	_			597
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Pro Trp Pro Thr Leu 20		Phe Gly Tyr (	Gly Leu Gln Cys 30	Phe
Ala Arg Tyr Pro Asp 35	His Met Lys 1	Arg His Asp	Phe Phe Lys Ser	Ala
Met Pro Glu Gly Tyr	Val Gln Glu 2	-	Phe Phe Lys Asp	Asp

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 105 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190 Gly Met Asp Glu Leu Tyr Lys 195 <210> 114 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; CFP F2A, N146I/M153T/V163A mutations <223> and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 114 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 30 20 25

ttc gcc cgc tac ccc Phe Ala Arg Tyr Pro 35				144
gcc atg ccc gaa ggc Ala Met Pro Glu Gly 50			e Phe Phe Lys Asp	192
gac ggc aac tac aag Asp Gly Asn Tyr Lys 65				240
ctg gtg aac cgc atc Leu Val Asn Arg Ile 85				288
aac atc ctg ggg cac Asn Ile Leu Gly His 100	Lys Leu Glu :			336
tat atc acc gcc gac Tyr Ile Thr Ala Asp 115				384
atc cgc cac aac atc Ile Arg His Asn Ile 130			u Ala Asp His Tyr	432
cag cag aac acc ccc Gln Gln Asn Thr Pro 145				480
cac tac ctg agc acc His Tyr Leu Ser Thr 165				528
cgc gat cac atg gtc Arg Asp His Met Val 180	Leu Leu Glu 1			576
ctc ggc atg gac gag Leu Gly Met Asp Glu 195				600
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<400> 115				
Met Gly Lys Leu Thr 1 5	Leu Lys Phe I	Ile Cys Thr Thi 10	r Gly Lys Leu Pro 15	

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 25 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210><211><211><212><213>	116 597 DNA Artif	: icia	al													
<220> <223>	modif mutat		_	; CG1	FP F:	2 <b>A</b> , 1	F46L,	/S65'	T/Y60	6W/N:	1461,	/M15:	3 <b>T/V</b> :	163A/	T203Y	
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ccc tgo Pro Tr																96
gcc cgc Ala Arc																144
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ggc aad Gly Asr 65																240
gtg aad Val Asr	c cgc n Arg	atc Ile	gag Glu 85	ctg Leu	aag Lys	ggc Gly	atc Ile	gac Asp 90	ttc Phe	aag Lys	gag Glu	gac Asp	ggc Gly 95	aac Asn		288
atc cto																336
atc acc																3'84
cgc cad Arg His	a Asn								Leu							432
cag aad Gln Asr 145																480
tac cto Tyr Lei	agc Ser	tac Tyr	cag Gln 165	tcc Ser	gcc Ala	ctg Leu	agc Ser	aaa Lys 170	gac Asp	ccc Pro	aac Asn	gag Glu	aag Lys 175	cgc Arg	!	528

gat Asp	cac His	atg Met	gtc Val 180	ctg Leu	ctg Leu	gag Glu	ttc Phe	gtg Val 185	acc Thr	gcc Ala	gcc Ala	ggg Gly	atc Ile 190	act Thr	ctc Leu	576
					tac Tyr											597
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Gly 1	Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Сув	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	•
Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Leu 25	Thr	Trp	Gly	Leu	Gln 30	Cys	Phe	
Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met	Pro 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	
Gly 65	Asn	Tyr	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val	Asn	Arg	Ile	Glu 85	Leu	Lys		Ile	_		Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Ile	Ser	His	Asn 110	Val	Tyr	
Ile	Thr	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 118 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag., CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 118 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys 20 25 30 tto goo ego tac eec gac cac atg aag egg cac gac tto tto aag tec 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac atc aqc cac aac qtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
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<pre>&lt;400&gt; 119  Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>	
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 Thr Leu Thr Thr Gly Lys Leu Gln Cys	
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 15  Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys 30  Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 Yal Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys 30 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 45 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys 30 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 45 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125
le Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140
In Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 45 150 155 160
lis Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175
arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190
eu Gly Met Asp Glu Leu Tyr Lys 195 200
210> 120 211> 597 212> DNA 213> Artificial
220> 223> modif. frag.; CGFP F2A, N146I/T203Y mutations
223> modif. frag.; CGFP F2A, N146I/T203Y mutations  220> 221> CDS
223> modif. frag.; CGFP F2A, N146I/T203Y mutations  220> 221> CDS 222> (1)(597)  400> 120 gc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 14 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
223> modif. frag.; CGFP F2A, N146I/T203Y mutations  220> 221> CDS 222> (1)(597)  400> 120 gc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 5 10 15  cc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc ro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
223> modif. frag.; CGFP F2A, N146I/T203Y mutations  220> 221> CDS 222> (1)(597)  400> 120 gc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 5 10 15  cc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc ro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30  cc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc la Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
223> modif. frag.; CGFP F2A, N146I/T203Y mutations  220> 221> CDS 222> (1)(597)  400> 120 gc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 ly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 5 10 15  cc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc ro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30  cc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc la Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45  tg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac et Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

	85		90	9	95
atc ctg ggg cac Ile Leu Gly His 100					
atc atg gcc gac Ile Met Ala Asp 115			Ile Lys Val		
cgc cac aac atc Arg His Asn Ile 130		y Ser Val			
cag aac acc ccc Gln Asn Thr Pro 145					
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ggc atg gac gag Gly Met Asp Glu 195		-			597
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Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Ile	Ser	His	Asn 110	Val	Tyr	
Ile	Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Val	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Ľeu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys									·	
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	ggc	122 aag Lys														48
		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192

50 55 60

gac ggc aac Asp Gly Asn 65	_				_
ctg gtg aac Leu Val Asn					
aac atc ctg			Asn Tyr I		
tat atc atg Tyr Ile Met . 115					
atc cgc cac Ile Arg His 130			. Val Gln I		
cag cag aac Gln Gln Asn 145					
cac tac ctg					
cgc gat cac			e Val Thr A		
ctc ggc atg ( Leu Gly Met 2 195		_			600
<210> 123 <211> 200 <212> PRT <213> Artif	icial				
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Val Pro Trp	Pro Thr Leu 20	Val Thr Thr 25	Phe Gly T	Tyr Gly Leu 30	Gln Cys
Phe Ala Arg '	Tyr Pro Asp	His Met Lys	Arg His A	Asp Phe Phe 45	Lys Ser

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 90 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 124 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, M153T/T203Y mutations <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

	20			25					30			٠
gcc cgc tac Ala Arg Tyr 35												144
atg ccc gaa Met Pro Glu 50												192
ggc aac tac Gly Asn Tyr 65												240
gtg aac cgc Val Asn Arg												288
atc ctg ggg Ile Leu Gly												336
atc acc gcc Ile Thr Ala 115												384
cgc cac aac Arg His Asn 130												432
cag aac acc Gln Asn Thr 145												480
tac ctg agc Tyr Leu Ser												528
gat cac atg Asp His Met	Val Leu		Phe	Val	Thr	Ala	Ala	${\tt Gly}$	Ile	Thr		576
ggc atg gac Gly Met Asp 195												597
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<220> <223> modi:	f. frag.;	; CGFP F	2A, M	11537	T/T2(	)3Y n	nutat	ions	3			
<400> 125					•							

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1  $\,$  5  $\,$  10  $\,$  15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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       modif. frag.; CGFP F2A, M153T/T203Y mutations + Met @ posit. 1
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Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                25
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                                                                      240
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
                            120
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                     170
                                                                      576
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
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ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200 600

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<211> 200

<212> PRT

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<220>

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

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ccc tg															96
gcc cg Ala Ar															144
atg cc Met Pr 50															192
ggc aa Gly As 65	c tac n Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240
gtg aa Val As															288
atc ct															336
atc ac	gcc Ala 115	gac Asp	aag Lys	cag Gln	aag Lys	aac Asn 120	ggc Gly	atc Ile	aag Lys	gtg Val	aac Asn 125	ttc Phe	aag Lys	atc Ile	384
cgc ca Arg Hi	s Asn														432

145	acc Thr														4	180
tac ctg Tyr Leu															5	528
gat cac Asp His															5	576
ggc atg Gly Met																597
	129 199 PRT Arti	ficia	al													
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Gly Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val		
Pro Trp	Pro		Leu	Val	Thr	Thr		Gly	Tyr	Gly	Leu		Cys	Phe		
		20					25					30				
Ala Arg	Tyr 35		Asp	His	Met	Lys 40		His	Asp	Phe	Phe 45		Ser	Ala		
Ala Arg	35	Pro	_			40	Arg				45	Lys	·			
Met Pro	35 Glu	Pro Gly	Tyr	Val	Gln 55	40 Glu	Arg Arg	Thr	Ile	Phe 60	45 Phe	Lys	Asp	Asp		
Met Pro 50	35 Glu Tyr	Pro Gly Lys	Tyr	Val Arg 70	Gln 55 Ala	40 Glu Glu	Arg Arg Val	Thr Lys	Ile Phe 75	Phe 60 Glu	45 Phe Gly	Lys Lys Asp	Asp Thr	Asp Leu 80		
Met Pro 50 Gly Asn 65	35 Glu Tyr Arg	Pro Gly Lys Ile	Tyr Thr Glu 85	Val Arg 70 Leu	Gln 55 Ala Lys	40 Glu Glu	Arg Arg Val	Thr Lys Asp 90	Ile Phe 75	Phe 60 Glu	45 Phe Gly Glu	Lys Lys Asp	Asp Thr Gly 95	Asp Leu 80 Asn		

130	Glu Asp	Gly Ser 135	Val Gln	Leu Ala 140	Asp His	Tyr	Gln
Gln Asn Thr Pro 145	Ile Gly 150	Asp Gly	Pro Val	Leu Leu 155	Pro Asp	Asn	His 160
Tyr Leu Ser Tyr	Gln Ser 165	Ala Leu	Ser Lys 170	Asp Pro	Asn Glu	Lys 175	Arg
Asp His Met Val	Leu Leu	Glu Phe	Val Thr 185	Ala Ala	Gly Ile 190	Thr	Leu
Gly Met Asp Glu 195	Leu Tyr	Lys					
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<220> <223> modif. f and Met	rag.; CGE added @ p		146I/ M1	53T/T203	Y mutatio	ons	
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<221> CDS <222> (1)(60  <400> 130 atg ggc aag ctg Met Gly Lys Leu 1  gtg ccc tgg ccc Val Pro Trp Pro 20  ttc gcc cgc tac Phe Ala Arg Tyr	acc ctc Thr Leu  ccc gac Pro Asp	Lys Phe gtg acc Val Thr cac atg His Met 40 gtc cag	Ile Cys 10 acc ttc Thr Phe 25 aag cgg Lys Arg	Thr Thr  ggc tac Gly Tyr  cac gac His Asp  acc atc	ggc ctg Gly Leu 30 ttc ttc Phe 45 ttc ttc	Leu 15 cag Gln aag Lys	Pro tgc 96 Cys tcc 144 Ser gac 192
<pre>&lt;221&gt; CDS &lt;222&gt; (1)(60  &lt;400&gt; 130 atg ggc aag ctg Met Gly Lys Leu 1  gtg ccc tgg ccc Val Pro Trp Pro</pre>	acc ctg Thr Leu 5  acc ctc Thr Leu ccc gac Pro Asp ggc tac Gly Tyr aag acc	Lys Phe gtg acc Val Thr  cac atg His Met 40 gtc cag Val Gln 55 cgc gcc	Ile Cys 10 acc ttc Thr Phe 25 aag cgg Lys Arg gag cgc Glu Arg gag gtg	Thr Thr  ggc tac Gly Tyr  cac gac His Asp  acc atc Thr Ile 60  aag ttc	ggc ctg Gly Leu 30  ttc ttc Phe Phe 45  ttc ttc Phe gag ggc	Leu 15 cag Gln aag Lys aag Lys	Pro tgc 96 Cys tcc 144 Ser gac 192 Asp

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110	336
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	

Leu Val	. Asn	Arg	11e 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn Ile	e Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Ile	Ser	His 110	Asn	Val	
Tyr Ile	Thr 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile Arg		Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln Glr 145	ı Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
<210><211><211><212><213>	132 597 DNA Arti	ficia	al												
<220> <223>	modi muta		_	; CGI	FP F:	2 <b>A</b> ,F6	54L/S	565T,	/Y66W	V/N14	161/1	<b>4153</b> 7	r/T2(	)3Y	
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ccc tgg Pro Trp															96
gcc cgc Ala Arg															144

			ggc Gly													192
			aag Lys													240
			atc Ile													288
			cac His 100													336
			gac Asp													384
			atc Ile													432
			ccc Pro													480
			tac Tyr													528
			gtc Val 180													576
			gag Glu	_		_										597
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<220 <223	3> r		f. fr	_	: CGI	FP F2	2A, E	F64L/	'S651	[/Y66	5W/N1	L46I,	/M153	3T/T2	203Y	
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Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Leu 25	Thr	Trp	Gly	Leú	Gln 30	Cys	Phe	

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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 mutations and Met added @ posit. 1

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Met 1	Gly	Lys	Leu	Thr 5	Leu	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
												ggc Gly				96
												ttc Phe 45				144
												ttc Phe				192
												gag Glu				240
												aag Lys				288
												agc Ser				336
												gtg Val 125				384
												gcc Ala			tac Tyr	432
												ctg Leu				480
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 mutations and Met added @ posit. 1

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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

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Leu Gly Met Asp Glu Leu Tyr Lys

165	170	175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195	597
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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160 THIS PAGE BLANK (USPTO)

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 138 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; CGFP F2A, V163A/T203Y mutations + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 138 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120

432

atc ege cae aac atc gag gac ggc age gtg cag etc gee gac cae tae

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140
cag cag aac acc ccc at Gln Gln Asn Thr Pro Il 145 15	e Gly Asp Gly Pro Val	
cac tac ctg agc tac ca His Tyr Leu Ser Tyr Gl 165		
cgc gat cac atg gtc ct Arg Asp His Met Val Le 180		
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Val Pro Trp Pro Thr Le	u Val Thr Thr Phe Gly 25	Tyr Gly Leu Gln Cys 30
Phe Ala Arg Tyr Pro As	o His Met Lys Arg His 40	Asp Phe Phe Lys Ser 45
Ala Met Pro Glu Gly Ty 50	r Val Gln Glu Arg Thr 55	Ile Phe Phe Lys Asp
Asp Gly Asn Tyr Lys Th	r Arg Ala Glu Val Lys 75	Phe Glu Gly Asp Thr 80
Leu Val Asn Arg Ile Gl 85	u Leu Lys Gly Ile Asp 90	Phe Lys Glu Asp Gly 95
Asn Ile Leu Gly His Ly 100	s Leu Glu Tyr Asn Tyr 105	Asn Ser His Asn Val
Tyr Ile Met Ala Asp Ly 115	s Gln Lys Asn Gly Ile 120	Lys Ala Asn Phe Lys 125

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
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1 5 10 15	
	96
1 5 10 15  ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc  Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30  gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	96
1 5 10 15  CCC tgg CCC acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30  gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45  atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	96 144
1 5 10 15  ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30  gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 45  atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50  ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	96 144 192

	100		105	110		
				gcc aac ttc Ala Asn Phe 125	_	84
				gcc gac cac Ala Asp His 140		32
	Pro Ile (			ctg ccc gac Leu Pro Asp		80
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ggc atg gac Gly Met Asp 195						97
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Ala Arg Tyr 35	Pro Asp 1	His Met Lys 40	Arg His Asp	Phe Phe Lys 45	Ser Ala	
Met Pro Glu 50	Gly Tyr '	Val Gln Glu 55	Arg Thr Ile	Phe Phe Lys	Asp Asp	
Gly Asn Tyr 65	_	Arg Ala Glu 70	Val Lys Phe 75	Glu Gly Asp	Thr Leu 80	

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 142 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, N146I/V163A/T203Y mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 142 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 tte gee ege tae eee gae eae atg aag egg eae gae tte tte aag tee 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50

gac ggc aa Asp Gly As 65											240
ctg gtg aa Leu Val As											288
aac atc ct Asn Ile Le				r Asn							336
tat atc at Tyr Ile Me	et Ala Asp										384
atc cgc ca Ile Arg Hi 130											432
cag cag aa Gln Gln As 145											480
cac tac ct His Tyr Le		Gln Ser									528
cgc gat ca Arg Asp Hi				e Val		_	_				576
ctc ggc at Leu Gly Me	t Asp Glu										600
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	lif. frag. I Met adde			6I/V1	53A/1	[203]	/ mut	atio	ons		
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Val Pro Tr	p Pro Thr 20	Leu Val	Thr Th		Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe Ala Ar		Asp His	Met Ly 40	s Arg	His	Asp	Phe 45	Phe	Lys	Ser	

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 144 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, M153T/V163A/T203Y mutations <220> <221> CDS <222> (1)..(597) <400> 144 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

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	ro Asp His Met 1		ttc ttc aag tcc Phe Phe Lys Ser 45	
			ttc ttc aag gac Phe Phe Lys Asp 60	
			gag ggc gac acc Glu Gly Asp Thr	
			aag gag gac ggc Lys Glu Asp Gly 95	
Ile Leu Gly Hi			agc cac aac gtc Ser His Asn Val 110	
	sp Lys Gln Lys <i>1</i>		gcc aac ttc aag Ala Asn Phe Lys 125	
cgc cac aac at Arg His Asn Il 130	tc gag gac ggc a le Glu Asp Gly 8 135	agc gtg cag ctc Ser Val Gln Leu	gcc gac cac tac Ala Asp His Tyr 140	cag 432 Gln
			ctg ccc gac aac Leu Pro Asp Asn	
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Asp His Met Va			gcc ggg atc act Ala Gly Ile Thr 190	
ggc atg gac ga Gly Met Asp Gl 195				597
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Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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       and Met added @ posit. 1
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gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                        96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                25
tto goo ogo tao ooo gao cao atg aag ogg cao gao tto tto aag too
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
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gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag
                                                                      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115
                            120
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
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Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 148 <211> 597 <212> DNA <213> Artificial <220> modif. frag.; CGFP F2A, N146I/M153T/V163A/T203Y mutations <220> <221> CDS <222> (1)..(597) <400> 148 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 144 gee ege tac eee gae cac atg aag egg cac gae tte tte aag tee gee Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 288 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120

432

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag

130	e Glu Asp	Gly Ser 135	Val Glr	Leu Ala 140	Asp His	Tyr	Gln
cag aac acc cc Gln Asn Thr Pro 145							
tac ctg agc ta Tyr Leu Ser Ty				Asp Pro			
gat cac atg gt Asp His Met Va 18	Leu Leu					e Thr	
ggc atg gac gac Gly Met Asp Gli 195							597
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Pro Trp Pro Th	Leu Val	Thr Thr	Phe Gly 25	Tyr Gly	Leu Glr 30		Phe
_			25		30	ı Cys	
20 Ala Arg Tyr Pro	Asp His	Met Lys 40	25	Asp Phe	Phe Lys	n Cys s Ser	Ala
Ala Arg Tyr Pro 35	Asp His Tyr Val	Met Lys 40 Gln Glu 55	Arg His	Asp Phe Ile Phe 60	Phe Lys 45	Cys Ser	Ala Asp
Ala Arg Tyr Pro 35  Met Pro Glu Gly So Gly Asn Tyr Lys	Asp His Tyr Val Thr Arg 70	Met Lys 40 Gln Glu 55 Ala Glu	Arg His	Asp Phe Ile Phe 60 Phe Glu 75	Phe Lys The Lys Gly Asp	Cys Ser Asp	Ala Asp Leu 80
Ala Arg Tyr Pro 35  Met Pro Glu Gly 50  Gly Asn Tyr Lys 65	Asp His Tyr Val Thr Arg 70 Glu Leu 85 Lys Leu	Met Lys 40 Gln Glu 55 Ala Glu Lys Gly	Arg His  Arg Thr  Val Lys  Ile Asp	Asp Phe Ile Phe 60 Phe Glu 75 Phe Lys	Phe Lys Gly Asp	Cys Ser Asp Thr Gly 95	Ala Asp Leu 80 Asn

130	Glu Asp	Gly Ser 135	Val Gln	Leu Ala 140	Asp His	Tyr	Gln
Gln Asn Thr Pro	Ile Gly 150	Asp Gly	Pro Val	Leu Leu 155	Pro Asp		His 160
Tyr Leu Ser Tyr	Gln Ser 165	Ala Leu	Ser Lys 170	Asp Pro	Asn Glu	Lys 175	Arg
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Gly Met Asp Glu 195	Leu Tyr	Lys					
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	rag.; CGE s and Met				A/T203Y		
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aac atc ctg Asn Ile Leu												336
tat atc acc Tyr Ile Thr 115												384
atc cgc cac Ile Arg His 130			Gly									432
cag cag aac Gln Gln Asn 145												480
cac tac ctg His Tyr Leu		-	_	_	_		_				_	528
cgc gat cac Arg Asp His												576
ctc ggc atg Leu Gly Met 195		_	_									600
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	5				10			-	-	15		
Met Gly Lys	Pro Thr 20	Leu Va	. Thr	Thr 25	10 Phe	Gly	Tyr	Gly	Leu 30	15 Gln	Cys	
Met Gly Lys 1 Val Pro Trp Phe Ala Arg	Pro Thr 20 Tyr Pro	Leu Val	Thr Met 40	Thr 25 Lys	10 Phe Arg	Gly His	Tyr Asp	Gly Phe 45	Leu 30	15 Gln Lys	Cys Ser	

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	·
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gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	144
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	192

	50					55					60					
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					ctg Leu											288
					ctg Leu											336
					cag Gln											384
					gac Asp											432
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					ctg Leu											576
	_	-		_	tac Tyr	_										597
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Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 154 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; BFP (blue) F2A, Y66H mutation and Met added <223> @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 154 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys 20 25 30

					gac Asp											144
					tac Tyr											192
gac Asp 65					acc Thr 70											240
					gag Glu											288
aac Asn					aag Lys											336
					aag Lys											384
					gag Glu											432
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cac His					cag Gln											528
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Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser
Ala	Met 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp
Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80
Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160
His	Tyr	Leu		Thr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200								

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ccc tqq ccc acc ctc qtq acc acc ttc qqc tac qqc ctq caq tqc ttc
                                                                        96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
                                 25
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50
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ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
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Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
                    70
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                       288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat
                                                                       336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
            100
                                 105
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc
                                                                       384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115
                             120
ege cac aac ate gag gae gge age gtg cag ete gee gae cac tae cag
                                                                       432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
                                                                       480
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                         155
                                                             160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
                                                                       528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165
                                     170
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc
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Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
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Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180  $\phantom{\bigg|}$  185  $\phantom{\bigg|}$  190  $\phantom{\bigg|}$ 

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		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192
gac Asp 65	ggc Gly	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
		aac Asn														288
		ctg Leu														336
tat Tyr	atc Ile	atg Met 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gtg Val 125	aac Asn	ttc Phe	aag Lys	384
		cac His														432

					atc Ile 150											480
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					ctg Leu											576
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Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala	Met 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Phe	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	<u>I</u> le	Lys	Val 125	Asn	Phe	Lys	

Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
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			Thr		gtg Val						ggc					96
			20					25	GIĀ	His	ĞĬy	Leu	Gln 30	Cys	Phe	
			CCC					25 cgg	cac	gac		ttc	30 aag	tcc	gcc	144
Ala	Arg	Tyr 35 gaa	ccc Pro	Asp	His gtc	Met cag	Lys 40 gag	cgg Arg	cac His	gac Asp atc	Gly	ttc Phe 45	aag Lys aag	tcc Ser	gcc Ala gac	144 192
Ala atg Met	acc	Tyr 35 gaa Glu tac	ccc Pro ggc Gly	Asp tac Tyr	His gtc Val cgc	Met cag Gln 55 gcc	Lys 40 gag Glu gag	cgc Arg gtg	cac His acc Thr	gac Asp atc Ile	Gly ttc Phe ttc Phe	ttc Phe 45 ttc Phe	aag Lys aag Lys gac	tcc Ser gac Asp	gcc Ala gac Asp	
Ala atg Met ggc Gly 65 gtg	CCC Pro 50 aac Asn	Tyr 35 gaa Glu tac Tyr	ccc Pro ggc Gly aag Lys	Asp tac Tyr acc Thr	His gtc Val cgc Arg 70	Met cag Gln 55 gcc Ala	Lys 40 gag Glu gag Glu	cgc Arg cgc Arg gtg Val	cac His acc Thr aag Lys	gac Asp atc Ile ttc Phe 75	Gly ttc Phe ttc Phe gag	ttc Phe 45 ttc Phe ggc Gly	aag Lys aag Lys gac Asp	tcc Ser gac Asp acc Thr	gcc Ala gac Asp ctg Leu 80	192

	100		105		110	
				aag gtg aac Lys Val Asn 125		
				ctc gcc gac Leu Ala Asp 140		
		Asp Gly		ctg ctg ccc Leu Leu Pro 155		
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gat cac atg Asp His Met						
ggc atg gac Gly Met Asp 195						597
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Pro Trp Pro	Thr Leu Val	Thr Thr		His Gly Leu	Gln Cvs	Phe
			25		30	
Ala Arg Tyr 35	Pro Asp His	Met Lys 40		Asp Phe Phe 45	30	Ala
		40	Arg His	45	30 Lys Ser	
35 Met Pro Glu	Gly Tyr Val	40 Gln Glu 55	Arg His	45 Ile Phe Phe 60	Lys Ser	Asp

100 105 110	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

ctg gtg a													288
aac atc o													336
tat atc a													384
atc cgc of Ile Arg I													432
cag cag a Gln Gln A 145			e Gly										480
cac tac o													528
cgc gat o Arg Asp I													576
ctc ggc a							٠						600
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Phe Ala A	Arg Tyr 35	Pro As	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala Met 1	Pro Glu	Gly Ty	Val	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	

Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80		•
Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly		
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Phe	Asn	Ser	His 110	Asn	Val		
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys		
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr		
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160		
His	Tyr	Leu	Ser	Thr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys		
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr		
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gcc	cgc	tac	çcc	gac	cac	atg	aag	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	:	144

Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
				tac Tyr												192
				acc Thr												240
				gag Glu 85												288
				aag Lys												336
				aag Lys												384
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Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Leu 25	Gly	His	Gly	Leu	Gln 30	Cys	Phe	

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

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ctg gt Leu Va															2	288
aac at Asn Il															3	336
tat at Tyr Il	_	_	_	_	_	_				_				_	3	384
atc cg Ile Ar 13	g His														4	132
cag ca Gln Gl 145															4	180
cac ta His Ty	_	_		_		_	_	_		_				_	Ę	528

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His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190 Leu Gly Met Asp Glu Leu Tyr Lys <210> 168 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; EGFP F2A, with Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 168 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys 20 25 tto tcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120

432

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

	120					125					140					
	130					135					140					
				ccc Pro												480
				tac Tyr 165												528
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		_	_	gag Glu	_		_									600
	l> 2 2> 1	169 200 PRT Artii	ficia	al												·
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Met 1	Gly	Lys							10					15	•	
Met 1 Val	Gly	Lys Trp	Pro 20	5	Leu	Val	Thr	Thr 25	10 Leu	Thr	Tyr	Gly	Val 30	15 Gln	Cys	
Met 1 Val	Gly Pro	Lys Trp Arg 35	Pro 20 Tyr	5 Thr	Leu Asp	Val His	Thr Met 40	Thr 25 Lys	10 Leu Arg	Thr His	Tyr Asp	Gly Phe 45	Val 30	15 Gln Lys	Cys Ser	
Met 1 Val Phe Ala	Gly Pro Ser Met 50	Lys Trp Arg 35 Pro	Pro 20 Tyr Glu	5 Thr Pro	Leu Asp Tyr	Val His Val 55	Thr Met 40	Thr 25 Lys Glu	10 Leu Arg	Thr His	Tyr Asp Ile	Gly Phe 45 Phe	Val 30 Phe	15 Gln Lys Lys	Cys Ser Asp	
Met 1 Val Phe Ala Asp 65	Gly Pro Ser Met 50	Lys Trp Arg 35 Pro	Pro 20 Tyr Glu	5 Thr Pro	Leu Asp Tyr Thr 70	Val His Val 55	Thr Met 40 Gln	Thr 25 Lys Glu	10 Leu Arg Arg	Thr His Thr Lys	Tyr Asp Ile 60 Phe	Gly Phe 45 Phe Glu	Val 30 Phe Phe	Gln Lys Lys Asp	Cys Ser Asp Thr	

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
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<400> 170 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
<pre>&lt;400&gt; 170 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1</pre>	6
<pre> &lt;400&gt; 170 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1</pre>	6
<pre> &lt;400&gt; 170 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1</pre>	6

atc (																336
atc a	Thr															384
cgc ( Arg I																432
cag a Gln 1 145																480
tac ( Tyr )																528
gat ( Asp I																576
ggc a	Met .															597
<210: <211: <212: <213:	> 1 > P	71 99 RT rtif	icia	ıl .												
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Gly I	Lys	Leu	Thr	Leu 5	_	Phe		-			_	_			Val	
Pro 9	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Phe 25	Thr	Tyr	Gly	Leu	Gln 30	Cys	Phe	
Ala A		Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met I	Pro ( 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Lys 110	Val	Tyr	
Ile	Thr	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Val	Asn 125	Phe	Lys	Thr	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
<210 <211 <212 <213	L> ( 2> 1	172 600 DNA Artif	icia	al											·	
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		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240							
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288							
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val 100 105 110	336							
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384							
acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432							
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480							
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528							
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576							
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600							
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys 20 25 30								
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45								

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val 100 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 120 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 174 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; YFP F2A, Y203F mutation <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

	20	2!	25	30	
gcc cgc tac Ala Arg Tyr 35					
atg ccc gaa Met Pro Glu 50			arg Thr Ile		
ggc aac tac Gly Asn Tyr 65	aag acc cgc Lys Thr Arg 70	gcc gag gt Ala Glu Va	gtg aag ttc Val Lys Phe 75	gag ggc gac Glu Gly Asp	acc ctg 240 Thr Leu 80
gtg aac cgc Val Asn Arg					
atc ctg ggg Ile Leu Gly		Glu Tyr As			
atc atg gcc Ile Met Ala 115					
cgc cac aac Arg His Asn 130			al Gln Leu .		
cag aac acc Gln Asn Thr 145					
tac ctg agc Tyr Leu Ser					
gat cac atg Asp His Met	gtc ctg ctg Val Leu Leu 180	Glu Phe Va	tg acc gcc ( al Thr Ala ) 85	gcc ggg atc Ala Gly Ile 190	act ctc 576 Thr Leu
ggc atg gac Gly Met Asp 195					597
<210> 175 <211> 199 <212> PRT <213> Artif	icial				
<220> <223> modif	f. frag.; YF	P F2A, Y203	3F mutation		
<400> 175					

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1  $\phantom{\bigg|}$  5

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

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       CDS
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                                                                       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                        55
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
                    70
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                                105
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
                            120
ate ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
                                                        175
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cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	76
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	

His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 178 <211> 597 <212> DNA <213> Artificial <220> modif. frag.; YFP F2A, Y203H mutation <223> <220> <221> CDS <222> (1)..(597) <400> 178 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115

432

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

130		135		140			
	ccc atc ggc Pro Ile Gly 150		Pro Val L				
	cac cag tcc His Gln Ser 165						
	gtc ctg ctg Val Leu Leu 180						
	gag ctg tac Glu Leu Tyr					597	
<210> 179 <211> 199 <212> PRT <213> Artis	ficial		·				
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Gly Lys Leu 1	Thr Leu Lys 5	Phe Ile	Cys Thr T	Thr Gly Lys	Leu Pro Val 15		
Pro Trp Pro	Thr Leu Val 20	Thr Thr	Phe Gly T 25	Tyr Gly Leu	Gln Cys Phe	4	
Ala Arg Tyr 35	Pro Asp His	Met Lys 40	Arg His A	Asp Phe Phe 45	Lys Ser Ala		
Met Pro Glu 50	Gly Tyr Val	Gln Glu 55	Arg Thr I	Ile Phe Phe 60	Lys Asp Asp		
Gly Asn Tyr 65	Lys Thr Arg 70	Ala Glu	_	Phe Glu Gly	Asp Thr Leu 80		
Val Asn Arg	Ile Glu Leu 85	Lys Gly	Ile Asp P	Phe Lys Glu	Asp Gly Asn 95		
Ile Leu Gly	His Lys Leu 100	Glu Tyr	Asn Tyr A	Asn Ser His	Asn Val Tyr 110		
Ile Met Ala 115	Asp Lys Gln	Lys Asn 120	Gly Ile L	ys Val Asn 125	Phe Lys Ile		

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160
Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190
Gly Met Asp Glu Leu Tyr Lys 195
<210> 180 <211> 600 <212> DNA <213> Artificial
<220> <223> modif. frag.; YFP F2A, Y203H mutation and Met added @ posit. 1
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<222> (1)(600)  <400> 180  atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
<pre>&lt;222&gt; (1)(600)  &lt;400&gt; 180  atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
<pre>&lt;222&gt; (1)(600)  &lt;400&gt; 180 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
<pre>&lt;222&gt; (1)(600)  &lt;400&gt; 180 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
<pre>&lt;222&gt; (1)(600)  &lt;400&gt; 180 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>

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			ggc atc aag gtg Gly Ile Lys Val 125	
	n Ile Glu A		gtg cag ctc gcc Val Gln Leu Ala 140	
			ccc gtg ctg ctg Pro Val Leu Leu 155	
		Ser Ala Leu	agc aaa gac ccc Ser Lys Asp Pro 170	
	t Val Leu I		gtg acc gcc gcc Val Thr Ala Ala	
ctc ggc atg ga Leu Gly Met As 195				600
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	frag.; YFP	F2A, Y203H	mutation and Met	added @ posit. 1
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Val Pro Trp Pro 20	o Thr Leu V	Val Thr Thr 25	Phe Gly Tyr Gly	Leu Gln Cys 30
Dha Na Nwa The				
35	r Pro Asp H	His Met Lys . 40	Arg His Asp Phe 45	Phe Lys Ser
35	ı Gly Tyr V	40	-	-
Ala Met Pro Gl	ם Gly Tyr V 5	40 Val Gln Glu .	45 Arg Thr Ile Phe	Phe Lys Asp

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
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gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30	96
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45	144
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	192

gac ggc a Asp Gly A 65		Lys '												240
ctg gtg a Leu Val A														288
aac atc c Asn Ile L														336
tat atc a Tyr Ile T 1														384
atc cgc c Ile Arg H 130														432
cag cag a Gln Gln A 145		Pro												480
cac tac c His Tyr L														528
cgc gat c Arg Asp H														576
ctc ggc a Leu Gly M 1														600
<210> 18 <211> 20 <212> PR <213> Ar	0	al												
	odif. fr et added				72A f	rag	(aa 4	10-23	39 of	E SEY	/FP,	with	n	
<400> 18	13													
Met Gly L	ys Leu	Thr 1	Leu	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val Pro T	rp Pro 20	Thr 1	Leu	Val	Thr	Thr 25	Leu	Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe Ala A	arg Tyr 5	Pro i	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 184 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; Venus F2A, with S175G mutation <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ecc tgg ecc acc etc gtg acc acc tte gge tac gge etg eag tge tte 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

2	20	25		30
	ccc gac cac atg Pro Asp His Met			
	ggc tac gtc cag Sly Tyr Val Gln 55			
	aag acc cgc gcc Lys Thr Arg Ala 70			
	atc gag ctg aag Ile Glu Leu Lys 85		p Phe Lys Glu	
Ile Leu Gly H	cac aag ctg gag His Lys Leu Glu .00	tac aac tac Tyr Asn Tyr 105	c aac agc cac r Asn Ser His	aac gtc tat 336 Asn Val Tyr 110
	gac aag cag aag Asp Lys Gln Lys			
	atc gag gac ggc Tle Glu Asp Gly 135	Gly Val Gl		
	ccc atc ggc gac Pro Ile Gly Asp 150			
	ac cag tcc gcc Tyr Gln Ser Ala 165		s Asp Pro Asn	
Asp His Met V	gtc ctg ctg gag Val Leu Leu Glu .80		r Ala Ala Gly	
	gag ctg tac aag Slu Leu Tyr Lys			597
<210> 185 <211> 199 <212> PRT <213> Artific	.cial			
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<400> 185				

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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

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<210> 186
 <211>
       600
<212>
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<213>
       Artificial
<220>
       modif. frag.; Venus F2A, with S175G mutation and Met
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       added @ posit. 1
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Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                        96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                 25
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                       144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                       192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                       240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65
                     70
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                       288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                 85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                       336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
             100
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                       384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
ate ege cae aac ate gag gae gge gge gtg cag ete gee gae cae tae
                                                                       432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
    130
                         135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                       480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg age tac cag tcc gcc ctg age aaa gac ccc aac gag aag
                                                                       528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                 165
                                     170
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ege gat cae atg gte etg gag tte gtg ace gee ggg ate act 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 ctc ggc atg gac gag ctg tac aag 600 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 187 <211> 200 <212> PRT <213> Artificial <220> <223> modif. frag.; Venus F2A, with S175G mutation and Met added @ posit. 1 <400> 187 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 188 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2A, with M153T, S175G mutations <220> <221> CDS <222> (1)..(597) <400> 188 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120

432

cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac tac cag

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln

130	135	140
cag aac acc ccc atc ggc Gln Asn Thr Pro Ile Gly 145	Asp Gly Pro Val Leu	
tac ctg agc tac cag tcc Tyr Leu Ser Tyr Gln Ser 165		
gat cac atg gtc ctg ctg Asp His Met Val Leu Leu 180		
ggc atg gac gag ctg tac Gly Met Asp Glu Leu Tyr 195		597
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Pro Trp Pro Thr Leu Val	Thr Thr Phe Gly Tyr 25	Gly Leu Gln Cys Phe 30
Ala Arg Tyr Pro Asp His	Met Lys Arg His Asp 40	Phe Phe Lys Ser Ala 45
Met Pro Glu Gly Tyr Val 50	. Gln Glu Arg Thr Ile 55	Phe Phe Lys Asp Asp 60
Gly Asn Tyr Lys Thr Arg	J Ala Glu Val Lys Phe 75	Glu Gly Asp Thr Leu 80
Val Asn Arg Ile Glu Leu 85	Lys Gly Ile Asp Phe 90	Lys Glu Asp Gly Asn 95
Ile Leu Gly His Lys Leu 100	Glu Tyr Asn Tyr Asn 105	Ser His Asn Val Tyr 110
Ile Thr Ala Asp Lys Glr 115	Lys Asn Gly Ile Lys 120	Val Asn Phe Lys Ile 125

Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Gly	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
	.> 6 ?> I	190 500 DNA Artif	icia	al												
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		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192
gac Asp 65	ggc Gly	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
		220	~~~		~~~	a+ ~	224	aac	ata	asa.	++0	226	~~~	<b>~</b> ~~		288
ctg Leu		Asn														200

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Thr 115	_											384
atc cgc cac Ile Arg His 130			Gly									432
cag cag aac Gln Gln Asn 145	acc ccc Thr Pro	atc ggo Ile Gly 150	gac Asp	ggc Gly	Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480
cac tac ctg His Tyr Leu												528
cgc gat cac Arg Asp His												576
ctc ggc atg Leu Gly Met 195	Asp Glu											600
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	f.frag.; d @ posi		'2A, N	M1537	C, S1	75G	muta	ation	ıs aı	nd Me	et	
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100 105 110	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
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<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; Venus F2A, with V163A, S175G mutations  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 192 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val</pre>	
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<pre>&lt;212&gt; DNA &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; Venus F2A, with V163A, S175G mutations  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(597)  &lt;400&gt; 192 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1</pre>	6

65	70	75	80
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		aac agc cac aac gtc Asn Ser His Asn Val	
		aag gcc aac ttc aag Lys Ala Asn Phe Lys 125	
		ctc gcc gac cac tac Leu Ala Asp His Tyr 140	
		ctg ctg ccc gac aac Leu Leu Pro Asp Asn 155	
	Ser Ala Leu Ser Lys	gac ccc aac gag aag Asp Pro Asn Glu Lys 175	
		gcc gcc ggg atc act Ala Ala Gly Ile Thr 190	
ggc atg gac gag ctg Gly Met Asp Glu Leu 195			597
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<220> <223> modif. frag.	; Venus F2A, with V1	63A, S175G mutations	
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Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Gly 25	Tyr Gly Leu Gln Cys	Phe
Ala Arg Tyr Pro Asp	His Met Lys Arg His	Asp Phe Phe Lys Ser 45	Ala
Met Pro Glu Gly Tyr	Val Gln Glu Arg Thr 55	Ile Phe Phe Lys Asp	Asp

Gly Asn Tyr Lys Thr Arq Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 194 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; Venus F2A, w. V163A, S175G mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 194 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

gcc atg Ala Met 50													192
gac ggc Asp Gly 65			r Arg										240
ctg gtg Leu Val													288
aac atc Asn Ile													336
tat atc Tyr Ile													384
atc cgc Ile Arg 130													432
cag cag Gln Gln 145			e Gly										480
cac tac His Tyr													528
cgc gat Arg Asp													576
ctc ggc Leu Gly													600
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	nodif. fi und Met a				w. \	71637	A, S1	L75G	muta	ation	ns		
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Met Gly	Lys Leu	Thr Le	u Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val Pro	Trp Pro 20	Thr Le	u Val	Thr	Thr 25	Phe	Gly	Tyr	Gly	Leu 30	Gln	Cys	

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 120 115 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 190 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 196 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2A,F46L/F64L/M153T/V163A/S175G mutations <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val

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	gac cac atg aag cgg Asp His Met Lys Arg 40		
	tac gtc cag gag cgc Tyr Val Gln Glu Arg 55		
	acc cgc gcc gag gtg Thr Arg Ala Glu Val 70		
	gag ctg aag ggc atc Glu Leu Lys Gly Ile 85		
	aag ctg gag tac aac Lys Leu Glu Tyr Asn 105		
	aag cag aag aac ggc Lys Gln Lys Asn Gly 120		
	gag gac ggc ggc gtg Glu Asp Gly Gly Val 135		
	atc ggc gac ggc ccc Ile Gly Asp Gly Pro 150		
	cag tcc gcc ctg agc Gln Ser Ala Leu Ser 165		
	ctg ctg gag ttc gtg Leu Leu Glu Phe Val 185		
ggc atg gac gag Gly Met Asp Glu 195			597
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<220> <223> modif. f:	rag.; Venus F2A,F46L/	F64L/M153T/V163A/S17	75G mutations
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Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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gtg Val	ccc	tgg Trp	ccc Pro 20	acc Thr	ctc Leu	gtg Val	acc Thr	acc Thr 25	ctc Leu	ggc Gly	tac Tyr	ggc Gly	ctg Leu 30	cag Gln	tgc Cys	96
		cgc Arg 35														144
gcc Ala	atg Met 50	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp	192
		aac Asn														240
		aac Asn														288
		ctg Leu														336
tat Tyr	atc Ile	acc Thr 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gcc Ala 125	aac Asn	ttc Phe	aag Lys	384
		cac His								Gln						432
		aac Asn														480
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		cac His														576
		atg Met 195														600
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Met 1	Gly	Lys	Leu	Thr 5	Leu	Lys	Leu	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val	Pro	Trp	Pro 20	Thr	Leu	Val	Thr	Thr 25	Leu	Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala	Met 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp 65	Gly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Thr 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Ala 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Gly	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	

165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 200 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1B (aa residues 1-103 of YFP) with posit. 1 Met removed <220> <221> CDS <222> (1)..(306) <400> 200 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 4.0 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cqq 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306 Thr Ile Phe Phe Lys Asp 100

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys

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<211> 102
<212> PRT
<213> Artificial
<220>
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                                  10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                               25
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                           40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                       55
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                  70
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
               85
                                   90
Thr Ile Phe Phe Lys Asp
           100
<210> 202
<211> 309
<212> DNA
<213> Artificial
<220>
<223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is
Τ,
      residue 69 is V, and residue 73 is S
<220>
<221> CDS
<222> (1)..(309)
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atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg
                                                                     48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
               5
```

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	6
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	4
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc  Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  50 55 60	2
ctc acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	0
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	8
cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	9
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<223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T, residue 69 is V, and residue 73 is S	
<223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is $T,$	
<pre>&lt;223&gt; modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,</pre>	
<pre>&lt;223&gt; modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,     residue 69 is V, and residue 73 is S &lt;400&gt; 203  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	
<pre> &lt;223&gt; modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,     residue 69 is V, and residue 73 is S  &lt;400&gt; 203  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	
<pre>c223&gt; modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,     residue 69 is V, and residue 73 is S  c400&gt; 203  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	

## Arg Thr Ile Phe Phe Lys Asp

<210> 204 <211> 306 <212> DNA <213> Artificial	
<220> <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 i T,     residue 69 is V, residue 73 is S, and posit. 1 Met has been removed	is
<220> <221> CDS <222> (1)(306)	
<pre>&lt;400&gt; 204 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15</pre>	48
gagctggacgtaaacggccacaagttcagcgtgtccggcgagGluLeuAspGlyAspValAspHisLysPheSerValSerGlyGlu202530	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	L44
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc  Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  50 55 60	192
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cgg Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	306

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<210> 205
 <211> 102
 <212> PRT
 <213> Artificial
 <220>
 <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is
       residue 69 is V, residue 73 is S, and posit. 1 Met has been
 removed
 <400> 205
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
               5
                                   10
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
                        55
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
                    70
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
Thr Ile Phe Phe Lys Asp
            100
<210> 206
<211> 309
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; YFP F1B with K79R mutation
<220>
<221> CDS
<222> (1)..(309)
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
                                                                      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

:	20	25	30	
	ggc gat gcc acc Gly Asp Ala Thr			
	ggc aag ctg ccc Gly Lys Leu Pro 55			
	ggc ctg cag tgc Gly Leu Gln Cys 70	Phe Ala Arg T		
cgg cac gac t Arg His Asp	ttc ttc aag tcc Phe Phe Lys Ser 85	gcc atg ccc g Ala Met Pro G 90	aa ggc tac gtc lu Gly Tyr Val	cag gag 288 Gln Glu 95
Arg Thr Ile 1	ttc ttc aag gac Phe Phe Lys Asp 100			309
<210> 207 <211> 103 <212> PRT <213> Artif	icial			
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<400> 207				
Met Val Ser I	Lys Gly Glu Glu 5	Leu Phe Thr G	ly Val Val Pro	Ile Leu 15
	Asp Gly Asp Val 20	Asn Gly His L 25	ys Phe Ser Val	Ser Gly
Glu Gly Glu ( 35	Gly Asp Ala Thr	Tyr Gly Lys L 40	eu Thr Leu Lys 45	Phe Ile
Cys Thr Thr (	Gly Lys Leu Pro 55	Val Pro Trp P	ro Thr Leu Val	Thr Thr
Phe Gly Tyr (	Gly Leu Gln Cys 70		yr Pro Asp His 5	Met Arg 80
Arg His Asp H	Phe Phe Lys Ser 85	Ala Met Pro G 90	lu Gly Tyr Val	Gln Glu 95

Arg Thr Ile Phe Phe Lys Asp 100

```
<210> 208
 <211>
       306
 <212> DNA
 <213> Artificial
 <220>
 <223> modif. frag.; YFP F1B with K79R mutation and
       posit. 1 Met removed
 <220>
 <221> CDS
 <222> (1)..(306)
 <400> 208
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                       48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
                                 25
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                      192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg
                                                                      240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
                                                                      288
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
 acc atc ttc ttc aag gac
                                                                      306
 Thr Ile Phe Phe Lys Asp
            100
<210> 209
 <211> 102
 <212> PRT
 <213> Artificial
 <220>
       modif. frag.; YFP F1B with K79R mutation and
       posit. 1 Met removed
 <400> 209
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

GI	, Giu	35	АБР	Ala	1111	ıyı	40	пуъ	ьеи	1111	Беи	45	FIIE	116	Суѕ	
Thi	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	
Gly 65	Tyr	Gly	Leu	Gln	Cys 70	Phe	Ala	Arg	Tyr	Pro 75	Asp	His	Met	Arg	Arg 80	
His	asp	Phe	Phe	Lys 85	Ser	Ala	Met	Pro	Glu 90	Gly	Tyr	Val	Gln	Glu 95	Arg	
Thi	lle	Phe	Phe 100	Lys	Asp											
	.1> .2>	210 309 DNA Arti:	ficia	al												
<22 <22		modi:	f. f	rag.	; YI	FP F	lB w	ith Y	766F	muta	atio	n				
<22 <22 <22	!1>	CDS	. (30	9)												
<40 ato Met	00> ggtg Val	210 agc Ser	aag Lys	ggc Gly 5	gag Glu	gag Glu	ctg Leu	ttc Phe	acc Thr 10	ggg Gly	gtg Val	gtg Val	ccc Pro	atc Ile 15	ctg Leu	48
	gag Glu															96
_	ggc Gly	_	_		_			_								1,44
	acc Thr 50															192
	ggc Gly															240
	cac His															288

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Arg Thr Ile Phe Phe Lys Asp
            100
<210> 211
<211>
      103
<212>
      PRT
<213> Artificial
<220>
<223> modif. frag.; YFP F1B with Y66F mutation
<400> 211
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                       55
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
               85
                                    90
Arg Thr Ile Phe Phe Lys Asp
           100
<210> 212
<211> 306
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; YFP F1B with Y66F mutation and
      posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(306)
<400> 212
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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cgc acc atc ttc ttc aag gac

1	5	10		15
	gac gta aac ggc Asp Val Asn Gly			
	gcc acc tac ggc Ala Thr Tyr Gly 40			
	ctg ccc gtg ccc Leu Pro Val Pro 55			
	cag tgc ttc gcc Gln Cys Phe Ala 70			
	aag tcc gcc atg Lys Ser Ala Met 85			
acc atc ttc ttc Thr Ile Phe Phe 100				306
<210> 213 <211> 102 <212> PRT <213> Artificia	al			
	rag.; YFP F1B w Met removed	ith Y66F muta	ition and	·
<400> 213				
Val Ser Lys Gly 1	Glu Glu Leu Phe 5	Thr Gly Val	Val Pro Ile	Leu Val 15
Glu Leu Asp Gly 20	Asp Val Asn Gly	His Lys Phe 25	Ser Val Ser 30	Gly Glu
Gly Glu Gly Asp 35	Ala Thr Tyr Gly 40	Lys Leu Thr	Leu Lys Phe 45	Ile Cys
Thr Thr Gly Lys	Leu Pro Val Pro 55	Trp Pro Thr	Leu Val Thr 60	Thr Phe
Gly Phe Gly Leu 65	Gln Cys Phe Ala 70	Arg Tyr Pro 75	Asp His Met	Lys Arg 80
His Asp Phe Phe	Ing Com No Mot	Pro Glu Gly	m 17-1 Cl-	01 h

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<210> 214
<211> 309
<212> DNA
<213> Artificial
<220>
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<220>
<221> CDS
<222> (1)..(309)
<400> 214
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                                                                      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                     96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac
                                                                     309
Arg Thr Ile Phe Phe Lys Asp
           100
<210> 215
<211> 103
<212> PRT
<213> Artificial
<223> modif. frag.; YFP F1B with Q69K mutation
<400> 215
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Thr Ile Phe Phe Lys Asp

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 20 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 100 <210> 216 <211> 306 <212> DNA <213> Artificial <220> modif. frag.; YFP F1B with Q69K mutation and <223> posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 216 gtg age aag gge gag gag etg tte ace ggg gtg gtg eee ate etg gte . 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 60 ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 306 acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100 <210> 217 <211> 102 <212> PRT <213> Artificial <220> <223> modif. frag.; YFP F1B with Q69K mutation and posit. 1 Met removed <400> 217 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 5 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 . 70 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85

Thr Ile Phe Phe Lys Asp

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<210>
       218
<211>
       309
<212>
       DNA
       Artificial
<213>
<220>
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       modif. frag.; YFP F1B with K79R mutation
<220>
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       CDS
<222>
       (1)..(309)
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                    10
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tte gge tae gge etg eag tge tte gee ege tae eee gae eae atg ege
                                                                      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65
                    70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
cgc acc atc ttc ttc aag gac
                                                                      309
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 219
<211> 103
<212>
      PRT
<213> Artificial
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      modif. frag.; YFP F1B with K79R mutation
<223>
<400>
     219
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                5
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 Arg Thr Ile Phe Phe Lys Asp 100 <210> 220 <211> 306 <212> DNA <213> Artificial <220> modif. frag.; YFP F1B with K79R mutation and <223> posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 220 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 70 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90

acc atc ttc ttc aag gac

Thr Ile Phe Phe Lys Asp 100 <210> 221 <211> 102 <212> PRT <213> Artificial <220> <223> modif. frag.; YFP F1B with K79R mutation and posit. 1 Met removed <400> 221 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 35 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 70 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

Thr Ile Phe Phe Lys Asp 100

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<211> 309
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; citrine F1B, with V68L, Q69M mutations

<220>
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<221> CDS
<222> (1)..(309)

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	309
<210> 223	
<211> 103 <212> PRT <213> Artificial	
<220> <223> modif. frag.; citrine F1B, with V68L, Q69M mutations	
<223> modif. frag.; citrine F1B, with V68L, Q69M mutations	
<223> modif. frag.; citrine F1B, with V68L, Q69M mutations <400> 223  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
<223> modif. frag.; citrine F1B, with V68L, Q69M mutations  <400> 223  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15  Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
<pre>&lt;223&gt; modif. frag.; citrine F1B, with V68L, Q69M mutations &lt;400&gt; 223  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	
<pre>&lt;223&gt; modif. frag.; citrine F1B, with V68L, Q69M mutations &lt;400&gt; 223  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	
<pre>&lt;223&gt; modif. frag.; citrine F1B, with V68L, Q69M mutations &lt;400&gt; 223  Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	

Arg Thr Ile Phe Phe Lys Asp

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<210> 224
 <211>
       306
 <212>
       DNA
 <213>
       Artificial
 <220>
 <223>
       modif. frag.; citrine F1B, with V68L, Q69M mutations
        and posit. 1 Met removed
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 <221> CDS
 <222> (1)..(306)
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                                                                       48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                       96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                 25
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                      144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                             40
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                      192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                         55
 ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                      240
 Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                                                                      288
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                                     90
 acc atc ttc ttc aag gac
                                                                      306
 Thr Ile Phe Phe Lys Asp
             100
<210> 225
 <211> 102
 <212> PRT
 <213> Artificial
 <220>
       modif. frag.; citrine F1B, with V68L, Q69M mutations
       and posit. 1 Met removed
 <400> 225
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                 5
                                     10
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

G	ly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Т	hr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	
G 6		Tyr	Gly	Leu	Met	Cys 70	Phe	Ala	Arg	Tyr	Pro 75	Asp	His	Met	Lys	Arg 80	
Н	is	Asp	Phe	Phe	Lys 85	Ser	Ala	Met	Pro	Glu 90	Gly	Tyr	Val	Gln	Glu 95	Arg	
T	hr	Ile	Phe	Phe 100	Lys	Asp											
< <		.> 3 ?> I	226 309 DNA Arti	ficia	al												
	220 223		nodi	f. fi	rag.	; Vei	nus I	F1B v	with	F461	J, F	54և ո	nutai	cions	3		•
<	220 221 222	.> (	CDS (1).	. (309	9)												
a		gtg					gag Glu										48
							gta Val										96
g G	ag lu	ggc Gly	gag Glu 35	ggc Gly	gat Asp	gcc Ala	acc Thr	tac Tyr 40	ggc Gly	aag Lys	ctg Leu	acc Thr	ctg Leu 45	aag Lys	ctg Leu	atc Ile	144
							ccc Pro 55										192
	eu						tgc Cys										240
C A	gg rg	cac His	gac Asp	ttc Phe	ttc Phe 85	aag Lys	tcc Ser	gcc Ala	atg Met	ccc Pro 90	gaa Glu	ggc Gly	tac Tyr	gtc Val	cag Gln 95	gag Glu	288

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100
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<211> 103
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<213> Artificial
<220>
<223> modif. frag.; Venus F1B with F46L, F64L mutations
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               5
                                   10
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                        55
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                   70
                                       75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
              85
                                   90
Arg Thr Ile Phe Phe Lys Asp
            100
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       and posit. 1 Met removed
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                                                                     48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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309

cgc acc atc ttc ttc aag gac

Arg Thr Ile Phe Phe Lys Asp

				5					10					15		
		gac Asp														96
		ggc Gly 35														144
		ggc Gly														192
		ggc Gly	_	_	_		_	_			_		_	_		240
		ttc Phe														288
		ttc Phe														306
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	3> n							vith	F46I	, F6	54L r	nutat	ions	5		
	3> π ε							vith	F46I	J, F6	54L r	nutat	cions	5		
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<223 <400 Val 1 Glu	3> m 5 5 Ser Leu Glu	Lys Asp	Gly Gly 20 Asp	Glu 5 Asp	Met Glu Val Thr	Leu Asn Tyr	Phe Gly Gly 40	Thr His 25 Lys	Gly 10 Lys Leu	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30 Leu	Leu 15 Gly Ile	Glu Cys	
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                                    90
cgc acc atc ttc ttc aag gac
                                                                      309
Arg Thr Ile Phe Phe Lys Asp
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Thr Ile Phe Phe Lys Asp

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

	u Asp Gly 20	Asp Val	Asn Gly 25	His Lys	Phe Ser	Val Se 30	r Gly	
Glu Gly Gl 35		Ala Thr	Tyr Gly 40	Lys Leu	Thr Leu 45	Lys Le	u Ile	
Cys Thr Th 50	r Gly Lys	Leu Pro 55	Val Pro	Trp Pro	Thr Leu 60	Val Th	r Thr	
Phe Gly Ty 65	r Gly Leu	Gln Cys 70	Phe Ala	Arg Tyr 75	Pro Asp	His Me	t Lys 80	• .
Arg His As	p Phe Phe 85	Lys Ser	Ala Met	Pro Glu 90	Gly Tyr	Val Gl 95		
Arg Thr Il	e Phe Phe 100	Lys Asp	·					
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	if. frag. it. 1 Met	·=	1B with	F46L muta	ation an	d		
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<223> mod pos <220> <221> CDS	it. 1 Met(306) g ggc gag	removed	ttc acc	ggg gtg	gtg ccc	atc ct		48
<223> mod pos  <220> <221> CDS <222> (1)  <400> 232 gtg agc aa Val Ser Ly	it. 1 Met(306) g ggc gag s Gly Glu 5 c ggc gac	gag ctg Glu Leu gta aac	ttc acc Phe Thr ggc cac	ggg gtg Gly Val 10	gtg ccc Val Pro	atc ct Ile Le 15	u Val c gag	<b>48</b> 96
<223> mod pos  <220> <221> CDS <222> (1)  <400> 232 gtg agc aa Val Ser Ly 1  gag ctg ga	it. 1 Met(306)  g ggc gag s Gly Glu 5 c ggc gac p Gly Asp 20 c gat gcc y Asp Ala	gag ctg Glu Leu gta aac Val Asn	ttc acc Phe Thr ggc cac Gly His 25 ggc aag	ggg gtg Gly Val 10 aag ttc Lys Phe	gtg ccc Val Pro agc gtg Ser Val	atc ct Ile Le 15 tcc gg Ser Gl 30 ctg at	u Val c gag y Glu c tgc	
<223> mod pos  <220> <221> CDS <222> (1)  <400> 232 gtg agc aa Val Ser Ly 1  gag ctg ga Glu Leu As  ggc gag gg Gly Glu Gl	it. 1 Met(306)  g ggc gag s Gly Glu 5 c ggc gac p Gly Asp 20 c gat gcc y Asp Ala c aag ctg	gag ctg Glu Leu gta aac Val Asn acc tac Thr Tyr	ttc acc Phe Thr  ggc cac Gly His 25  ggc aag Gly Lys 40  ccc tgg	ggg gtg Gly Val 10 aag ttc Lys Phe ctg acc Leu Thr	gtg ccc Val Pro agc gtg Ser Val ctg aag Leu Lys 45	atc ct Ile Le 15 tcc gg Ser Gl 30 ctg at Leu Il	c gag y Glu c tgc e Cys	96

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306 Thr Ile Phe Phe Lys Asp 100 <210> 233 <211> 102 <212> PRT <213> Artificial <220> <223> modif. frag.; YFP F1B with F46L mutation and posit. 1 Met removed <400> 233 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ·20 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90

Thr Ile Phe Phe Lys Asp 100

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                    10
                                                                       .96
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                        55
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                   .70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte cag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
                                    90
cgc acc atc ttc ttc aag gac
                                                                      309
Arq Thr Ile Phe Phe Lys Asp
            100
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<211> 103
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      PRT
      Artificial
<213>
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<223>
<400>
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                5
                                                         15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 90 Arg Thr Ile Phe Phe Lys Asp 100 <210> 236 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1B with F64L mutation and posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 236 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306

Thr Ile Phe Phe Lys Asp

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                               25
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                           40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                   70
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
               85
                   90
Thr Ile Phe Phe Lys Asp
           100
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<212> DNA
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                                                                     48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                                                     96
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys 35 40	2 2	14
tgc acc acc ggc aag ctg ccc gtg ccc tgg Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 50 55		92
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg 65 70		40
cgg cac gac ttc ttc aag tcc gcc atg ccc Arg His Asp Phe Phe Lys Ser Ala Met Pro 85 90		88
cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	30	9
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<220> <223> modif. frag.; CFP F1B with Y66W	mutation	
<400> 239	•	
<pre>&lt;400&gt; 239  Met Val Ser Lys Gly Glu Glu Leu Phe Thr 1</pre>	Gly Val Val Pro Ile Leu 15	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr	15	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr 1 5 Val Glu Leu Asp Gly Asp Val Asn Gly His	15 Lys Phe Ser Val Ser Gly 30	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr 10  Val Glu Leu Asp Gly Asp Val Asn Gly His 25  Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys	Lys Phe Ser Val Ser Gly 30  Leu Thr Leu Lys Phe Ile 45	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr 10  Val Glu Leu Asp Gly Asp Val Asn Gly His 25  Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Cys Thr Thr Gly Lys Leu Pro Val Pro Trp	Lys Phe Ser Val Ser Gly 30  Leu Thr Leu Lys Phe Ile 45  Pro Thr Leu Val Thr Thr 60	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr 10  Val Glu Leu Asp Gly Asp Val Asn Gly His 25  Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys 40  Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 55  Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg	Lys Phe Ser Val Ser Gly 30  Leu Thr Leu Lys Phe Ile 45  Pro Thr Leu Val Thr Thr 60  Tyr Pro Asp His Met Lys 80	

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       306
<212>
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      Artificial
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                    10
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50
                        55
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                    70
65
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
                                                                      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
acc atc ttc ttc aag gac
                                                                      306
Thr Ile Phe Phe Lys Asp
            100
<210> 241
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      102
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      PRT
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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                                    10
                                                         15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 60 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 90 Thr Ile Phe Phe Lys Asp 100 <210> 242 <211> 309 <212> DNA <213> Artificial <223> modif. frag.; CFP F1B with S65A mutation <220> <221> CDS <222> (1)..(309) <400> 242 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 309 cgc acc atc ttc ttc aag gac

Arg Thr Ile Phe Phe Lys Asp

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
                                        75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
Arg Thr Ile Phe Phe Lys Asp
<210> 244
<211> 306
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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20 25 30

Gly Glu Gly 35	gat gcc Asp Ala											144
acc acc ggc Thr Thr Gly 50						Thr I						192
gcc tac ggc Ala Tyr Gly 65					Tyr I							240
cac gac ttc His Asp Phe												288
acc atc ttc Thr Ile Phe												306
<210> 245 <211> 102 <212> PRT <213> Arti:	ficial											
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<220>									_			removed
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<220> <223> modi <400> 245 Val Ser Lys 1	Gly Glu 5 Gly Asp 20	Glu Leu Val Asn	Phe	Thr His 25	Gly \ 10 Lys I	Val V	Val Ser	Pro Val	Ile Ser 30	Leu 15 Gly	Val Glu	removed
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Thr Ile Phe Phe Lys Asp

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

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<213> Artificial
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      CDS
<222>
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
                                    90
cgc acc atc ttc ttc aag gac
                                                                     309
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 247
<211> 103
<212> PRT
<213> Artificial
<220>
<223>
      modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 100 <210> 248 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations, and posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 248 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys ace ace gge aag etg eee gtg eee tgg eee ace ete gtg ace ace tte 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

40

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306
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 Thr Ile Phe Phe Lys Asp
             100
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        102
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        PRT
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        Artificial
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        modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations,
        and posit. 1 Met removed
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 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
             20
                                 25
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
         35
                             40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
     50
                         55
 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                     70
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 Thr Ile Phe Phe Lys Asp
             100
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 <212> DNA
 <213> Artificial
        modif. frag.; CFP F1B, F64L , S65T, and Y66W mutations
 <220>
 <221>
       CDS
 <222> (1)..(309)
 <400> 250
 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1	5	10	15
		ggc cac aag ttc agc Gly His Lys Phe Ser 25	
		ggc aag ctg acc ctg Gly Lys Leu Thr Leu 45	
		ccc tgg ccc acc ctc Pro Trp Pro Thr Leu V 60	
		gcc cgc tac ccc gac Ala Arg Tyr Pro Asp 75	
		atg ccc gaa ggc tac Met Pro Glu Gly Tyr 90	
cgc acc atc ttc Arg Thr Ile Phe 100			309
<210> 251 <211> 103 <212> PRT			
<213> Artificia	al		
<213> Artificia <220>		4L ,S65T, and Y66W mu	ntations
<213> Artificia <220>		4L ,S65T, and Y66W mu	ntations
<213> Artificial <220> <223> modif. f: <400> 251  Met Val Ser Lys	rag.; CFP F1B,F6	4L ,S65T, and Y66W mu Phe Thr Gly Val Val 10	
<213> Artificial <220> <223> modif. f: <400> 251  Met Val Ser Lys 1	rag.; CFP F1B,F6 Gly Glu Glu Leu 5	Phe Thr Gly Val Val	Pro Ile Leu 15
<213> Artificial <220> <223> modif. fr <400> 251  Met Val Ser Lys 1  Val Glu Leu Asp 20	rag.; CFP F1B,F6 Gly Glu Glu Leu 5 Gly Asp Val Asn	Phe Thr Gly Val Val 10 Gly His Lys Phe Ser	Pro Ile Leu 15 Val Ser Gly 30
<213> Artificial <220> <223> modif. fr <400> 251  Met Val Ser Lys 1  Val Glu Leu Asp 20  Glu Gly Glu Gly 35	rag.; CFP F1B,F6 Gly Glu Glu Leu 5 Gly Asp Val Asn Asp Ala Thr Tyr 40	Phe Thr Gly Val Val 10 Gly His Lys Phe Ser 25 Gly Lys Leu Thr Leu	Pro Ile Leu 15 Val Ser Gly 30 Lys Phe Ile
<213> Artificial <220> <223> modif. fr <400> 251  Met Val Ser Lys 1  Val Glu Leu Asp 20  Glu Gly Glu Gly 35  Cys Thr Thr Gly 50	Gly Glu Glu Leu  Gly Asp Val Asn  Asp Ala Thr Tyr  40  Lys Leu Pro Val  55	Phe Thr Gly Val Val 10 Ser 25 Leu Thr Leu 45 Pro Trp Pro Thr Leu	Pro Ile Leu 15  Val Ser Gly 30  Lys Phe Ile  Val Thr Thr

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Arg Thr Ile Phe Phe Lys Asp
            100
<210>
       252
<211>
       306
<212>
       DNA
<213>
       Artificial
<220>
<223>
       modif. frag.; CFP F1B, F64L , S65T, and Y66W mutations,
       and posit. 1 Met removed
<220>
<221>
       CDS
<222>
      (1)..(306)
<400> 252
gtg age aag gge gag gag etg tte ace ggg gtg gtg eec ate etg gte
                                                                        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                     10
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc
                                                                       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
                        55
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                       240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65
                    70
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
                                                                       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
acc atc ttc ttc aag gac
                                                                       306
Thr Ile Phe Phe Lys Asp
            100
<210>
       253
<211>
       102
<212>
       PRT
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<210> 253
<211> 102
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations, and posit. 1 Met removed
<400> 253
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 55 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq Thr Ile Phe Phe Lys Asp 100 <210> 254 <211> 309 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1B, with Y66H mutation <220> <221> CDS <222> (1)..(309) <400> 254 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

288

cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100

309

<210> 255

<211> 103

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1B, with Y66H mutation

<400> 255

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp 100

<210> 256

<211> 306

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1B, with Y66H mutation and posit. 1 Met removed

<220> <221> CDS <222> (1)	. (306)				
		ctg ttc acc Leu Phe Thr			eu Val
		aac ggc cac Asn Gly His 25			
ggc gag ggc Gly Glu Gly 35	gat gcc acc Asp Ala Thr	tac ggc aag Tyr Gly Lys 40	ctg acc ctg Leu Thr Lei	g aag ttc at u Lys Phe II 45	cc tgc 144 le Cys
		gtg ccc tgg Val Pro Trp 55		u Val Thr Th	
		ttc gcc cgc Phe Ala Arg			
		gcc atg ccc Ala Met Pro			lu Arg
acc atc ttc Thr Ile Phe					306
<210> 257 <211> 102 <212> PRT <213> Artif	icial				
37	f. frag.; BF	P F1B, with	Y66H mutatio	on and posit	. 1
<400> 257					
Val Ser Lys 1	Gly Glu Glu 5	Leu Phe Thr	Gly Val Val	l Pro Ile Le	
Glu Leu Asp	Gly Asp Val 20	Asn Gly His 25	Lys Phe Ser	r Val Ser Gl 30	y Glu
Gly Glu Gly 35	Asp Ala Thr	Tyr Gly Lys	Leu Thr Leu	u Lys Phe Il 45	e Cys
Thr Thr Gly 50	Lys Leu Pro	Val Pro Trp 55	Pro Thr Let		nr Phe

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp 100 <210> 258 <211> 309 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1B, with F64L, Y66H mutations <220> <221> CDS <222> (1):.(309)<400> 258 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 90 cgc acc atc ttc ttc aag gac 309 Arg Thr Ile Phe Phe Lys Asp 100

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

70

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<210> 259
 <211> 103
 <212> PRT
 <213>
       Artificial
 <220>
       modif. frag.; BFP F1B, with F64L, Y66H mutations
 <400> 259
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                     70
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                 85
Arg Thr Ile Phe Phe Lys Asp
             100
 <210> 260
 <211> 306
 <212> DNA
 <213> Artificial
· <220>
 <223>
       modif. frag.; BFP F1B, with F64L, Y66H mutations
        and posit. 1 Met removed
 <220>
 <221>
       CDS
 <222>
        (1)..(306)
 <400> 260
 gtg age aag ggc gag gag etg tte ace ggg gtg gtg eec ate etg gte
                                                                        48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                     10
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
             20
                                 25
```

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	4
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg  Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  50  55  60	2
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	0
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	8
acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	6
<210> 261 <211> 102 <212> PRT <213> Artificial	
<220> <223> modif. frag.; BFP F1B, with F64L, Y66H mutations and posit. 1 Met removed	
400 000	
<400> 261	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15  Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15  Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20  Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15  Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20  Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 45  Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15  Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20  Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40  Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 55  Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	

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<210> 262
<211>
      411
<212>
      DNA
      Artificial
<213>
<220>
<223>
      modif. frag.; YFP F2B (aa residues 104-240 of EYFP)
       and Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(411)
<400> 262
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                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                                    10
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc
                                                                      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                                        75
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                                    90
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
                                                125
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210>
      263
<211>
      137
<212>
      PRT
<213>
      Artificial
<220>
<223>
      modif. frag.; YFP F2B (aa residues 104-240 of EYFP)
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and Met added @ posit. 1

<400> 263

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 264

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations  $\left(\frac{1}{2}\right)$ 

<220>

<221> CDS

<222> (1)..(408)

<400> 264

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

2.0	25	3.0
2.11	2.3	311

					aag Lys											144
					aag Lys											192
					gag Glu 70											240
					atc Ile											288
					cag Gln											336
					ctg Leu											384
					ctg Leu											408
<210 <211 <212 <213	.> 1 ?> I	265 136 PRT Artii	ficia	al .							·					
<220 <223 muta			E. fi	rag.	; EGI	FP F2	2B(en	mera]	ld),	N146	5K, N	<b>/153</b> 7	r, ar	nd II	L67T	
<400	)> 2	265														
Asp 1	Gly	Asn	Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly	
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Asn	Ser 45	His	Lys	Val	
Tyr	Ile 50	Thr	Ala	Asp	Lys	Gln 55	Lys	Asn	Gly	Ile	Lys 60	Val	Asn	Phe	Lys	
Thr 65	Arg	His	Asn	Ile	Glu 70	Asp	Gly	Ser	Val	Gln 75	Leu	Ala	Asp	His	Tyr 80	

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 90 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 125 Leu Gly Met Asp Glu Leu Tyr Lys <210> 266 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 266 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 10 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys gtc tat atc acc gcc gac aag cag aag ggc atc aag gtg aac ttc 192 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 aag acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu

110

105

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 120 1,15 act ctc ggc atg gac gag ctg tac aag 411 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 267 <211> 137 <212> PRT <213> Artificial <220> <223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations and Met added @ posit. 1 <400> 267 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys

135

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<210> 268
<211>
      408
<212> DNA
<213>
      Artificial
<220>
<223>
       modif. frag.; YFP F2B with Y203F mutation
<220>
<221>
       CDS
<222>
       (1)..(408)
<400> 268
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
                                    10
                                                                       96
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35
                            40
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50
                        55
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                    70
                                                             80
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg age ttc cag tcc gcc ctg age aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
ege gat eac atg gte etg etg gag tte gtg ace gee gee ggg ate act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115
                            120
ctc ggc atg gac gag ctg tac aag
                                                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 269
<211> 136
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; YFP F2B with Y203F mutation
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<400> 269
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85
                                    90
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 270
<211>
      411
<212> DNA
<213> Artificial
<220>
<223>
      modif. frag.; YFP F2B with Y203F mutation + Met @ posit. 1
<220>
<221>
      CDS
<222>
      (1)..(411)
<400> 270
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                       48
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96

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

5

35	c ctg ggg e Leu Gly										144
gtc tat ato Val Tyr Ilo 50		Asp L									192
aag atc cg Lys Ile Arg 65											240
tac cag cag Tyr Gln Gl				Asp (							288
aac cac tac Asn His Ty											336
aag cgc ga Lys Arg As 11!	His Met										384
act ctc ggo Thr Leu Gl 130		Glu I									411
010 : 071			*								
<210> 271 <211> 137 <212> PRT <213> Art	ificial										
<211> 137 <212> PRT <213> Art:	ificial	; YFP	F2B wit	h Y20	03F mui	cation	ı + N	Met @	) pos	sit. 1	
<211> 137 <212> PRT <213> Art:		; YFP	F2B wit	h Y20	03F mui	cation	ı + N	Met @	) pos	sit. 1	
<211> 137 <212> PRT <213> Art: <220> <223> mod:	lf. frag			Ala (							
<211> 137 <212> PRT <213> Art <220> <223> mod <400> 271  Met Asp Gl	if. frag / Asn Tyr 5	Lys I	Thr Arg	Ala (	Glu Vai	l Lys	Phe	Glu	Gly 15	Asp	
<211> 137 <212> PRT <213> Art: <220> <223> mod: <400> 271  Met Asp Gly 1	Asn Tyr 5 Asn Arg 20	Lys I	Thr Arg	Ala (	Glu Vai 10 Gly Ile	l Lys	Phe Phe	Glu Lys 30	Gly 15 Glu	Asp	
<pre>&lt;211&gt; 137 &lt;212&gt; PRT &lt;213&gt; Art &lt;220&gt; &lt;223&gt; mod &lt;400&gt; 271 Met Asp Gl 1  Thr Leu Va Gly Asn Ile</pre>	Asn Tyr 5  Asn Arc 20	Lys To the Good His L	Thr Arg	Ala (Lys (25)	Glu Va 10 Gly Ile Tyr Ası	l Lys e Asp n Tyr	Phe Phe Asn 45	Glu Lys 30	Gly 15 Glu His	Asp Asp Asn	

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 272 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2B with Y203H mutation <220> <221> CDS <222> (1)..(408) <400> 272 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 80 cag cag aac acc ccc atc ggc gac ggc ccc qtq ctq ctq ccc qac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 cac tac ctg age cac cag tee gee etg age aaa gae eee aae gag aag 336 His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggg atc act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

408

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys

130 135

<210> 273

<211> 136 <212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203H mutation

<400> 273

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 55

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 70 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn - 85 90

His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 . 125

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 274

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203H mutation + Met @ posit. 1

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       CDS
<222>
       (1)...(411)
<400> 274
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                                    10
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
                                25
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
                            40
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc
                                                                      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                    70
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 275
<211> 137
<212>
      PRT
<213> Artificial
<220>
       modif. frag.; YFP F2B with Y203H mutation + Met @ posit. 1
<223>
<400>
      275
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                5
                                    10
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 40 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 55 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 276 <211> 408 <212> DNA <213> Artificial <223> modif. frag.; CFP F2B with N146I mutation <220> <221> CDS <222> (1)..(408) <400> 276 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 5 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 55 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

75 70 75 80

					atc Ile												288
					cag Gln												336
					ctg Leu												384
					ctg Leu												408
<210 <211 <212 <213	L> : 2> :I	277 136 PRT Artii	Ficia	al												•	
<220 <223		nodi	E. fi	rag.;	: CFI	P F2E	3 wit	h Ni	L46I	muta	ation	1					
<400	)> 2	277	-														
Asp 1	Gly	Asn	Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr		
Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly		
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Ile	Ser 45	His	Asn	Val		
Tyr	Ile 50	Met	Ala	Asp	Lys	Gln 55	Lys	Asn	Gly	Ile	Lys 60	Val	Asn	Phe	Lys		
Ile 65	Arg	His	Asn	Ile	Glu 70	Asp	Gly	Ser	Val	Gln 75	Leu	Ala	Asp	His	Tyr 80		
Gln	Gln	Asn	Thr	Pro 85	Ile	Gly	Asp	Gly	Pro 90	Val	Leu	Leu	Pro	Asp 95	Asn		•
His	Tyr	Leu	Ser 100	Thr	Gln	Ser	Ala	Leu 105	Ser	Lys	Asp	Pro	Asn 110	Glu	Lys		
Arg	Asp	His	Met	Val	Leu	Leu	Glu 120	Phe	Val	Thr	Ala	Ala 125	Gly	Ile	Thr		

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<210> 278
<211> 411
<212> DNA
<213> Artificial
<220>
      modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1
<220>
<221>
      CDS
<222>
      (1)...(411)
<400> 278
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35
                            40
gtc tat atc atg gcc gac aag cag aag ggc atc aag gtg aac ttc
                                                                     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 279
<211> 137
<212> PRT
<213> Artificial
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Leu Gly Met Asp Glu Leu Tyr Lys

130

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<220>
<223> modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1
<400> 279
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
                                25
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                                        75
                    70
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
                                    90
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
       115
                            120
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 280
<211> 408
<212> DNA
<213> Artificial
<223> modif. frag.; CFP F2B with M153T mutation
<220>
<221> CDS
<222> (1)..(408)
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
                5
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      96
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

20		25	30
		tac aac tac aac ag Tyr Asn Tyr Asn Se 45	er His Asn Val
		aac ggc atc aag gt Asn Gly Ile Lys Va 60	
		agc gtg cag ctc gc Ser Val Gln Leu Al 75	
		ggc ccc gtg ctg ct Gly Pro Val Leu Le 90	
		ctg agc aaa gac co Leu Ser Lys Asp Pr 105	
		ttc gtg acc gcc gc Phe Val Thr Ala Al 12	a Gly Ile Thr
ctc ggc atg gac ga Leu Gly Met Asp Gl 130			408
<210> 281 <211> 136 <212> PRT <213> Artificial			
<220> <223> modif. frag	.; CFP F2B wi	th M153T mutation	
<400> 281			
Asp Gly Asn Tyr Ly 1 5	s Thr Arg Ala	Glu Val Lys Phe Gl	u Gly Asp Thr 15
Leu Val Asn Arg Il 20	e Glu Leu Lys	Gly Ile Asp Phe Ly 25	rs Glu Asp Gly 30
Asn Ile Leu Gly Hi 35	s Lys Leu Glu 40	Tyr Asn Tyr Asn Se	
Tyr Ile Thr Ala As	p Lys Gln Lys 55	Asn Gly Ile Lys Va	l Asn Phe Lys

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 282 <211> 411 <212> DNA <213> Artificial <223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 282 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 gto tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 aac cac tac ctg age acc cag tee gee etg age aaa gac eee aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile

115 120 125

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130
                        135
<210> 283
<211> 137
<212>
      PRT
<213> Artificial
<220>
<223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1
<400> 283
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
                       55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
           100
                                105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                       135
<210> 284
<211> 408
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; CFP F2B with N146I, M153T mutations
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411

act ctc ggc atg gac gag ctg tac aag

Thr Leu Gly Met Asp Glu Leu Tyr Lys

<220> <221> CDS <222> (1).	. (408)			
			gtg aag ttc gag Val Lys Phe Glu 10	
			atc gac ttc aag Ile Asp Phe Lys	
			aac tac atc agc Asn Tyr Ile Ser 45	
			ggc atc aag gtg Gly Ile Lys Val 60	
			gtg cag ctc gcc Val Gln Leu Ala 75	
			ccc gtg ctg ctg Pro Val Leu Leu 90	
			agc aaa gac ccc Ser Lys Asp Pro	
	Met Val Leu		gtg acc gcc gcc Val Thr Ala Ala 125	
	gac gag ctg Asp Glu Leu			408
<210> 285 <211> 136 <212> PRT <213> Arti	ficial			
<220> <223> modi	f. frag.; CF	P F2B with N1	146I, M153T mutat	cions
<400> 285			·	
Asp Gly Asn	Tyr Lys Thr 5	Arg Ala Glu	Val Lys Phe Glu 10	Gly Asp Thr 15
Leu Val Asn	Arg Ile Glu 20	Leu Lys Gly 25	Ile Asp Phe Lys	Glu Asp Gly 30

35 40 45	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 55 60	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	
Leu Gly Met Asp Glu Leu Tyr Lys 130 135	
<210> 286 <211> 411 <212> DNA <213> Artificial	
<220> <223> modif. frag.; CFP F2B with N146I, M153T mutations and Met added @ posit. 1	
<220> <221> CDS	
<222> (1)(411)	
<400> 286	48
<pre>&lt;400&gt; 286 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15</pre>	48 96
<pre>&lt;400&gt; 286 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1</pre>	
<pre>&lt;400&gt; 286 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1</pre>	96

65 70 75 80

		cag Gln															288
		tac Tyr															336
		gat Asp 115															384
		ggc Gly															411
	1> : 2> :	287 137 PRT Arti:	ficia	al													
<22 <22	3 > r	modi: and 1						h Ni	1461,	, M15	53 <b>T</b> r	nutat	ions	3		-	
<40	0> 2	287															
Met 1	Asp	Gly	Asn	Tyr 5	Lys	Thr	Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp		
Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp		
Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn		
Val	Tyr 50	Ile	Thr	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Val	Asn	Phe		
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80		
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp		
Asn	His	Tyr	Leu 100	Ser	Thr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu		
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile		

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Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135
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<210> 288 <211> 408 <212> DNA <213> Artificial	
<220> <223> modif. frag.; CFP F2B with V163A mutation	
<220> <221> CDS <222> (1)(408)	
<pre>&lt;400&gt; 288 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15</pre>	48
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45	144
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	240
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	384
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408
<210> 289 <211> 136 <212> PRT <213> Artificial	

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<223> modif. frag.; CFP F2B with V163A mutation
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                                25
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                            40
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                                        75
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
               85
                                    90
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
       115
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 290
<211> 411
<212> DNA
<213> Artificial
<223> modif. frag.; CFP F2B w. V163A mutation and Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(411)
<400> 290
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                5
1
                                    10
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
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<220>

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35 40 45	144
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cacLys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His65707580	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
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<212> PRT <213> Artificial  <220> <223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pc <400> 291  Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	osit. 1
<pre>&lt;212&gt; PRT &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F2B w. V163A mutation and Met added @ pc &lt;400&gt; 291  Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15</pre> Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	osit. 1
<pre>&lt;212&gt; PRT &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F2B w. V163A mutation and Met added @ pc &lt;400&gt; 291  Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1</pre>	osit. 1

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 292 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, V163A mutations <220> <221> CDS <222> (1)..(408) <400> 292 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 ate ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae 240 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag 336 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 408

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<220>

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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 294

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acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc
                                                                     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
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      and Met added @ posit. 1
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp

GIY	ASII	35	ьеи	GIY	пів	цув	40	Giu	TÀT	ASII	тĀт	45	ser	пів	ASII	
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Thr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
Thr	Leu 130	Gly	Met	Asp	Glu	Leu 135	Tyr	Lys								
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	gtg Val															96
	atc Ile															144
	atc Ile 50															192

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Ty 65 70 75 80	240 r
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp As:	
cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aa His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Ly 100 105 110	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc ac Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Th 115 120 125	
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp The 1 5 10 15	r ·
1 5 10 15  Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gl	Y
1 5 10 15  Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 25 30  Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Va	y 1
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 25  Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Va 45  Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	Y 1
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Va 45  Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50  Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	y l
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asp Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Va Ash Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50  Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 60  Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tys 65  Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp	y 1 S

Leu Gly Met Asp Glu Leu Tyr Lys 130 135	
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ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144
gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
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<212> PRT

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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 300

<211> 408

<212> DNA

<213> Artificial

-22N-

<223> modif. frag.; CFP F2B , N146I, M153T, and V163A mutations

<220>

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aac atc ctg c Asn Ile Leu C 35					
tat atc acc of Tyr Ile Thr 150				/s Ala Asn	
atc cgc cac a Ile Arg His A 65					
cag cag aac a Gln Gln Asn 1				eu Leu Pro	
cac tac ctg a	-		Ser Lys As		
cgc gat cac a Arg Asp His N 115					
ctc ggc atg c Leu Gly Met <i>I</i> 130		_			408
<210> 301 <211> 136 <212> PRT <213> Artifi	icial				
<220> <223> modif.	. frag.; CFI	P F2B , N146	I, M153T, a	and V163A m	utations
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Leu Val Asn A	Arg Ile Glu 20	Leu Lys Gly 25	lle Asp Ph	ne Lys Glu 30	Asp Gly
Asn Ile Leu 0 35	Gly His Lys	Leu Glu Tyr 40	Asn Tyr Il	e Ser His	Asn Val

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys

65 70 75 80	yr )
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp As 85 90 95	sn
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Ly 100 105 110	rs
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Th	ır
Leu Gly Met Asp Glu Leu Tyr Lys 130 135	
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<221> CDS <222> (1)(411)	
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<pre>&lt;222&gt; (1)(411)  &lt;400&gt; 302 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	96 96 96 96 96 96 96 96 96 96 96 96 96 9
<pre>&lt;222&gt; (1)(411)  &lt;400&gt; 302 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	96 96 96 96 97 97 97 97 97 97 97 97 97 97 97 97 97
<pre>&lt;222&gt; (1)(411)  &lt;400&gt; 302 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	96 96 96 96 96 97 98 98 98 98 98 98 98 98 98 98 98 98 98

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336												
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384												
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411												
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30													
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45													
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60													
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80													
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95													
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110													
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125													
Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135													

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<210>
       304
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       408
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       DNA
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ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                                25
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
        35
                            40
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50
                        55
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcg ggg atc act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115
                            120
ctc ggc atg gac gag ctg tac aag
                                                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
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       modif. frag.; CGFP F2B, w. N146I, T203Y mutations
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Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
	tat Tyr 50															192
	atc Ile															240

	ıc cag r Gln															288
	c cac n His															336
	g cgc 's Arg															384
	t ctc r Leu 130	Gly														411
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Th	ır Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp	
Gl	y Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
Va	ıl Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn		Ile 60	Lys	Val	Asn	Phe	
<b>Ьу</b> 65	s Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80	
Ту	r Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
As	n His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lу	s Arg	Asp	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	

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Thr Leu Gly Met Asp Glu Leu Tyr Lys
   130
                       135
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		aac Asn														96
		ctg Leu 35														144
		acc Thr													aag Lys	192
		cac His														240
		aac Asn														288
		ctg Leu														336
		cac His 115														384
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

48

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp

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gtc tat atc acc gcc gac Val Tyr Ile Thr Ala Asp 50			
aag atc cgc cac aac atc Lys Ile Arg His Asn Ile 65 70			
tac cag cag aac acc ccc Tyr Gln Gln Asn Thr Pro 85			
aac cac tac ctg agc tac Asn His Tyr Leu Ser Tyr 100			
aag cgc gat cac atg gtc Lys Arg Asp His Met Val 115			
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Thr Leu Val Asn Arg Ile 20	Glu Leu Lys Gly 25	Ile Asp Phe Lys 30	Glu Asp
Gly Asn Ile Leu Gly His	T - T - G1 - M		
35	40	Asn Tyr Asn Ser 45	His Asn
Val Tyr Ile Thr Ala Asp	40	45	

	n Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	·
Asn Hi	s Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys Ar	g Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
Thr Le		Met	Asp	Glu	Leu 135	Tyr	Lys								
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ctg gt Leu Va	g aac l Asn	cgc Arg 20	atc Ile	gag Glu	ctg Leu	aag Lys	ggc Gly 25	atc Ile	gac Asp	ttc Phe	aag Lys	gag Glu 30	gac Asp	ggc Gly	96
aac at					ctg	qaq	tac								
Asn Il	35	GIÀ	His	Lys	Leu										144
tat at Tyr Il 50	35 c acc	gcc	gac	aag	cag	Glu 40 aag	Tyr	Asn ggc	Tyr atc	Ile aag	Ser 45 gtg	His aac	Asn ttc	Val	144
tat at Tyr Il	35 c acc e Thr	gcc Ala aac	gac Asp atc	aag Lys gag	cag Gln 55 gac	Glu 40 aag Lys ggc	Tyr aac Asn agc	Asn ggc Gly gtg	Tyr atc Ile cag	aag Lys 60	Ser 45 gtg Val gcc	His aac Asn	Asn ttc Phe cac	Val aag Lys tac	
tat at Tyr Il 50 atc cg Ile Ar	35 c acc e Thr c cac g His	gcc Ala aac Asn	gac Asp atc Ile	aag Lys gag Glu 70 atc	cag Gln 55 gac Asp	Glu 40 aag Lys ggc Gly	Tyr aac Asn agc ser	Asn ggc Gly gtg Val	Tyr atc Ile cag Gln 75 gtg	aag Lys 60 ctc Leu	ser 45 gtg Val gcc Ala	His aac Asn gac Asp	Asn ttc Phe cac His	Val  aag Lys  tac Tyr 80  aac	192

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384 Arg Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 ctc ggc atg gac gag ctg tac aag 408 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 313 <211> 136 <212> PRT <213> Artificial <220> <223> modif. frag.; CGFP F2B, N146I, M153T, and T203Y mutations <400> 313 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 5 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 25 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 55 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 314 <211> 411

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 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                        96
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                       144
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc
                                                                       192
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
     50
                         55
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                       240
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                     70
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                       288
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                       336
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                 105
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                       384
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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                             120
 act ctc qqc atg qac qag ctg tac aag
                                                                       411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
     130
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

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aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

35

40

45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	240
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	384
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408
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Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 318 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2B, w. V163A, T203Y mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 318 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 55 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 75 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125 act ctc ggc atg gac gag ctg tac aag 411 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

120

115

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Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
   50 55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
          100
                               105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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                          120
Thr Leu Gly Met Asp Glu Leu Tyr Lys
   130
                       135
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					gag Glu											96
					aag Lys	_						_			-	144
					aag Lys											192
					gag Glu 70											240
					atc Ile											288
cac His	tac Tyr	ctg Leu	agc Ser 100	tac Tyr	cag Gln	tcc Ser	gcc Ala	ctg Leu 105	agc Ser	aaa Lys	gac Asp	ccc Pro	aac Asn 110	gag Glu	aag Lys	336
					ctg Leu										act Thr	384
		_	_		ctg Leu		_									408
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<400	)> 3	321								•						
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Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly	
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Ile	Ser 45	His	Asn	Val	

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 55 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 322 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2B, N146I, V163A, and T203Y mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411)<400> 322 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctq qtq aac cqc atc qaq ctq aaq qqc atc qac ttc aaq qaq qac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 gtc tat atc atg gcc gac aag cag aac ggc atc aag gcc aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65

		cag Gln														288
		tac Tyr														336
		gat Asp 115														384
		ggc Gly														411
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<400	0> 3	323														·
Met 1	Asp	Gly	Asn	Tyr 5	Lys	Thr	Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp	
Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu-	Asp	
Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	

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Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
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                                                                      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                                25
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                     144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                                                                     192
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
                        55
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                     240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                    70
                                        75
caq caq aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                     288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
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					cag Gln			Ser				336
					ctg Leu							384
ctc	ggc	atg	gac	gag	ctg	tac	aag					408

90

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 325 <211> 136 <212> PRT <213> Artificial

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Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
                   55
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                                   90
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
           100
                               105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
                           120
Leu Gly Met Asp Glu Leu Tyr Lys
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      and Met added @ posit. 1
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
               5
                                                       15
                                   10
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acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 \ 30	96
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144
gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cacLys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His65707580	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	

65 70 75	sp His 80
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pr 85 90 95	
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro As 100 105 110	sn Glu
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gl 115 120 125	y Ile
Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	
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<pre>&lt;400&gt; 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	p Thr c ggc 96 p Gly c gtc 144
<pre>&lt;400&gt; 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	c ggc 96 p Gly c gtc 144 n Val
<pre>&lt;400&gt; 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	c ggc 96 p Gly c gtc 144 n Val c aag 192 e Lys c tac 240

cac tac ctg age tac cag tee gee ctg age aaa gae eee aac gag aag 336 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 ctc ggc atg gac gag ctg tac aag 408 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 329 <211> 136 <212> PRT<213> Artificial <220> <223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations <400> 329 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 95 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 Leu Gly Met Asp Glu Leu Tyr Lys

135

130

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       and Met added @ posit. 1
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atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35
gtc tat atc acc gcc gac aag cag aag ggc atc aag gcc aac ttc
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Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
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Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                    70
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggq atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
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and Met added @ posit. 1

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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
                        55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                                   90
               85
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                               105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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Thr Leu Gly Met Asp Glu Leu Tyr Lys
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                       135
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<223> modif. frag.; BFP F2B with Y145F mutation
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tat atc a Tyr Ile M 50														192
atc cgc c Ile Arg H 65														240
cag cag a														288
cac tac c His Tyr I														336
cgc gat c Arg Asp H														384
ctc ggc a Leu Gly M 130			_		_									408
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Leu Val A	sn Arg 20		Glu				10	_				15		
Asn Ile I	20	Ile		Leu	Lys	Gly 25	10	Asp	Phe	Lys	Glu 30	15 Asp	Gly	
Asn Ile I	20 eu Gly 5	Ile His	Lys	Leu Leu	Lys Glu 40	Gly 25 Tyr	10 Ile Asn	Asp Phe	Phe Asn	Lys Ser 45	Glu 30	15 Asp Asn	Gly Val	

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 90 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 334 <211> 411 <212> DNA <213> Artificial <223> modif. frag.; BFP F2B w. Y145F mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 334 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc qac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn 35 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile

115 120 125

act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys

130 135

411

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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 336

<211> 408

<212> DNA

<213> Artificial

<220>

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ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                        55
atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
ege gat cae atg gte etg etg gag tte gtg ace gee gee ggg ate act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115
                            120
                                                                      408
ctc ggc atg gac gag ctg tac aag
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 337
<211>
      136
      PRT
<212>
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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25

20

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 115 125 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 338 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2B with S175G mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 338 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn gtc tat atc atg gcc gac aag cag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50

240

aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His 65 70 75 80

tac Tyr	cag Gln	cag Gln	aac Asn	acc Thr 85	ccc Pro	atc Ile	ggc Gly	gac Asp	ggc Gly 90	ccc Pro	gtg Val	ctg Leu	ctg Leu	ccc Pro 95	gac Asp	288
					tac Tyr											336
					gtc Val											384
					gag Glu											411
	1> : 2> :		ficia	al												
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Met 1	Asp	Gly	Asn	Tyr 5	Lys	Thr	Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp	
Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp	
Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Asn 45	Ser	His	Asn	
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Val	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Gly	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	

## Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 340 <211> 408 <212> DNA <213> Artif	11> 408 12> DNA											
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ctg gtg aac Leu Val Asn						96						
aac atc ctg ( Asn Ile Leu 35						144						
tat atc acc of Tyr Ile Thr .						192						
atc cgc cac Ile Arg His 65						240						
cag cag aac Gln Gln Asn						288						
cac tac ctg			Ser Lys			336						
cgc gat cac a Arg Asp His 1	atg gtc ctg Met Val Leu	ctg gag ttc Leu Glu Phe 120	gtg acc Val Thr	gcc gcc ggg Ala Ala Gly 125	atc act Ile Thr	384						
ctc ggc atg Leu Gly Met 130						408						
<210> 341 <211> 136 <212> PRT <213> Artif	icial											

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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                            40
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
                    70
                                        75
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
               85
                                    90
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
       115
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
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<212> DNA
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      and Met added @ posit. 1
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
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3	Chr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp		
						cac His												144
						gac Asp												192
Ι						atc Ile 70												240
						ccc Pro												288
						tac Tyr												336
						gtc Val												384
						gag Glu												411
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1	Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp		
G	Sly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Asn 45	Ser	His	Asn		
V	/al	Tyr 50	Ile	Thr	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Val	Asn	Phe		

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His

65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 344 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2B w. V163A, S175G mutations <220> <221> CDS <222> (1)..(408) <400> 344 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac tac 240 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 70 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 408

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Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

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## and Met added @ posit. 1

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ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144									
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192									
aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cacLys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His65707580	240									
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288									
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336									
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384									
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411									
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp

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Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Gly	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
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					gag Glu											96
					aag Lys											144
					aag Lys											192

	cgc Arg															240
	cag Gln															288
	tac Tyr															336
cgc Arg	gat Asp	cac His 115	atg Met	gtc Val	ctg Leu	ctg Leu	gag Glu 120	ttc Phe	gtg Val	acc Thr	gcc Ala	gcc Ala 125	ggg ggg	atc Ile	act Thr	384
	ggc Gly 130															408
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•	0> 3 Gly		Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Asp 1		Asn	_	5				•	10	-			-	15	÷	
Asp 1 Leu	Gly	Asn Asn	Arg 20	5 Ile	Glu	Leu	Lys	Gly 25	10	Asp	Phe	Lys	Glu 30	15 Asp	Gly	
Asp 1 Leu Asn	Gly	Asn Leu 35	Arg 20	5 Ile His	Glu Lys	Leu	Lys Glu 40	Gly 25 Tyr	10 Ile Asn	Asp Tyr	Phe Asn	Lys Ser 45	Glu 30	Asp Asn	Gly Val	
Asp 1 Leu Asn	Gly Val Ile	Asn Leu 35	Arg 20 Gly Ala	Ile His Asp	Glu Lys Lys	Leu Leu Gln 55	Lys Glu 40 Lys	Gly 25 Tyr Asn	10 Ile Asn Gly	Asp Tyr	Phe Asn Lys 60	Lys Ser 45	Glu 30 His	Asp Asn Phe	Gly Val Lys	
Asp 1 Leu Asn Tyr Ile 65	Gly Val Ile Ile 50	Asn Leu 35 Thr	Arg 20 Gly Ala Asn	Ile His Asp	Glu Lys Lys Glu 70	Leu Leu Gln 55	Lys Glu 40 Lys	Gly 25 Tyr Asn	10 Ile Asn Gly Val	Asp Tyr Ile Gln 75	Phe Asn Lys 60	Lys Ser 45 Ala	Glu 30 His Asn	Asp Asn Phe	Gly Val Lys Tyr 80	

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125

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       and Met added @ posit. 1
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acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
                                25
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35
gtc tat atc acc gcc gac aag cag aac ggc atc aag gcc aac ttc
                                                                      192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50
aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Val Gln Leu Ala Asp His
65
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210> 351
<211>
      137
<212> PRT
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Leu Gly Met Asp Glu Leu Tyr Lys

<213> Artificial <220> <223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations and Met added @ posit. 1 <400> 351 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 5 · 15 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 55 Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 352 <211> 348 <212> DNA <213> Artificial

<220>
<223> modif. frag.; YFP F1C (aa residues 1-117 of EYFP) with
 posit.1 Met removed

<220>
<221> CDS
<222> (1)..(348)
<400> 352

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

1	5	10	=	15
gag ctg gac ggc Glu Leu Asp Gly 20				
ggc gag ggc gat Gly Glu Gly Asp 35				
acc acc ggc aag Thr Thr Gly Lys 50				
ggc tac ggc ctg Gly Tyr Gly Leu 65				
cac gac ttc ttc His Asp Phe Phe			Tyr Val Gln (	
acc atc ttc ttc Thr Ile Phe Phe 100				
aag ttc gag ggc Lys Phe Glu Gly 115				348
<210> 353 <211> 116 <212> PRT <213> Artificia	al			
	rag.; YFP F1C (a	aa residues 1	-117 of EYFP)	with
<400> 353			•	
Val Ser Lys Gly	Glu Glu Leu Pho 5	e Thr Gly Val 10	_	Geu Val 15
Glu Leu Asp Gly 20	Asp Val Asn Gly	y His Lys Phe 25	Ser Val Ser 0 30	Gly Glu
Gly Glu Gly Asp 35	Ala Thr Tyr Gly	y Lys Leu Thr	Leu Lys Phe 1 45	Ile Cys
Thr Thr Gly Lys 50	Leu Pro Val Pro 55	Trp Pro Thr	Leu Val Thr 1	Thr Phe
Gly Tyr Gly Leu 65	Gln Cys Phe Ala	Arg Tyr Pro	Asp His Met I	ys Arg 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq 85

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105

Lys Phe Glu Gly 115

<210> 354 <211> 351

<212> DNA <213> Artificial

<220>

<223> modif. frag.; YFP F1C, with F46L mutation

<220>

<221> CDS

<222> (1)..(351)

<400> 354

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 80

egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105

gtg aag ttc gag ggc 351

Val Lys Phe Glu Gly 115

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<212> PRT
<213> Artificial
<223> modif. frag.; YFP F1C, with F46L mutation
<400> 355
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                   10
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                        55
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
<210> 356
<211> 348
<212> DNA
<213> Artificial
<223> modif. frag.; YFP F1C w. F46L mutation & posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(348)
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
```

<211> 117

20		25	30	
ggc gag ggc gat g Gly Glu Gly Asp A 35		Lys Leu Thr Leu		
acc acc ggc aag c Thr Thr Gly Lys L 50				
ggc tac ggc ctg c Gly Tyr Gly Leu G 65				
cac gac ttc ttc a His Asp Phe Phe L 8				
acc atc ttc ttc a Thr Ile Phe Phe L 100				
aag ttc gag ggc Lys Phe Glu Gly 115			,	348
<210> 357 <211> 116 <212> PRT <213> Artificial				
<220> <223> modif. fra	ng.; YFP F1C w.	F46L mutation &	posit. 1 Met	removed
<400> 357				
Val Ser Lys Gly G 1 5		Thr Gly Val Val	Pro Ile Leu 15	Val
Glu Leu Asp Gly A 20	sp Val Asn Gly	His Lys Phe Ser	Val Ser Gly 30	Glu
Gly Glu Gly Asp A 35	Ala Thr Tyr Gly 40		Lys Leu Ile 45	Суѕ
Thr Thr Gly Lys L 50	Leu Pro Val Pro 55	Trp Pro Thr Leu 60	Val Thr Thr	Phe
Gly Tyr Gly Leu G 65	Gln Cys Phe Ala 70	Arg Tyr Pro Asp 75	His Met Lys	Arg 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Lys Phe Glu Gly 115 <210> 358 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1C with K79R mutation <220> <221> CDS <222> (1)..(351)<400> 358 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 70 65 288 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag Arq His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 95 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

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<213> Artificial
<220>
 <223> modif. frag.; YFP F1C with K79R mutation
 <400> 359
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
                     70
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                 85
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 Val Lys Phe Glu Gly
         115
 <210> 360
 <211>
        348
 <212> DNA
 <213> Artificial
 <223> modif. frag.; YFP F1C w. K79R mutation & posit. 1 Met removed
 <220>
 <221> CDS
 <222> (1)..(348)
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                       48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                     10
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<210> 359 <211> 117 <212> PRT

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gl 20 25 30	gc gag 96 ly Glu
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc at Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe II 35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc ac Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Th 50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met An 65 70 75	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag ga His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln G 85 90 95	lu Arg
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc ga Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Gl 100 105 110	
aag ttc gag ggc Lys Phe Glu Gly 115	348
<210> 361 <211> 116 <212> PRT <213> Artificial	·
<220> <223> modif. frag.; YFP F1C w. K79R mutation & posit. 1	Met removed
<400> 361	
<pre>Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Le 1</pre>	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Le	5
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Le 1 5 10 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gl	5 ly Glu
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Le 19   Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe II	iy Glu le Cys

85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 362 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1C with Y66F mutation <220> <221> CDS <222> (1)..(351) <400> 362 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc qqc ttc qqc ctq caq tqc ttc qcc cqc tac ccc qac cac atq aaq 240 Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu 95 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly 115

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

90

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<211> 117
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; YFP F1C with Y66F mutation
<400> 363
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                               25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                           40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
           100
                        105
Val Lys Phe Glu Gly
       115
<210> 364
<211>
      348
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; YFP F1C w. Y66F mutation & posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(348)
<400> 364
gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                     96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
```

20		25	30	٠
			aag ttc atc tgc 14 Lys Phe Ile Cys 45	144
			gtg acc acc ttc 19 Val Thr Thr Phe	192
			cac atg aag cgg 24 His Met Lys Arg 80	240
His Asp Phe Phe			gtc cag gag cgc 28 Val Gln Glu Arg 95	288
			cgc gcc gag gtg 33 Arg Ala Glu Val 110	336
aag ttc gag ggc Lys Phe Glu Gly 115			. 34	348
<210> 365 <211> 116 <212> PRT <213> Artificia	1			
<220> <223> modif. fr	ag.; YFP F1C w.	Y66F mutation &	posit. 1 Met removed	l
<400> 365				
Val Ser Lys Gly	Glu Glu Leu Phe 5	Thr Gly Val Val	Pro Ile Leu Val 15	
Glu Leu Asp Gly . 20	Asp Val Asn Gly	His Lys Phe Ser 25	Val Ser Gly Glu 30	
Gly Glu Gly Asp . 35	Ala Thr Tyr Gly 40	Lys Leu Thr Leu	Lys Phe Ile Cys 45	
Thr Thr Gly Lys	Leu Pro Val Pro 55	Trp Pro Thr Leu 60	Val Thr Thr Phe	
Gly Phe Gly Leu 65	Gln Cys Phe Ala 70	Arg Tyr Pro Asp 75	His Met Lys Arg 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Lys Phe Glu Gly 115 <210> 366 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1C with Q69K mutation <220> <221> CDS <222> (1)..(351) <400> 366 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 ege ace ate the the aag gae gae gge aac tac aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

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<211>
      117
<212>
      PRT
<213>
      Artificial
<220>
<223> modif. frag.; YFP F1C with Q69K mutation
<400> 367
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                        55
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                                        75
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                                105
Val Lys Phe Glu Gly
        115
<210>
      368
<211> 348
<212> DNA
<213> Artificial
<220>
<223>
      modif. frag.; YFP F1C w. Q69K mutation & posit. 1 Met removed
<220>
      CDS
<221>
<222> (1)..(348)
<400> 368
gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                    10
```

		gac Asp														96
		ggc Gly 35														144
		ggc Gly														192
		ggc Gly														240
		ttc Phe														288
		ttc Phe														336
		gag Glu 115														348
<210 <211 <211 <211	1> : 2> :	369 116 PRT Artii	ficia	al												
<220 <220		modii	. fi	rag.	YFI	P F10	w.	Q69I	( mut	atio	on &	posi	.t. 1	L Met	removed	
<40	O> 3	369														
Val	Ser															
1	oci	Lys	Gly	Glu 5	Glu	Leu	Phe	Thr	Gly 10	Val	Val	Pro	Ile	Leu 15	Val	
1		Lys	_	5					10					15		
1 Glu	Leu	_	Gly 20	5 Asp	Val	Asn	Gly	His 25	10 Lys	Phe	Ser	Val	Ser 30	15 Gly	Glu	
1 Glu Gly	Leu Glu	Asp	Gly 20	5 Asp Ala	Val Thr	Asn Tyr	Gly Gly 40	His 25 Lys	Lys	Phe Thr	Ser	Val Lys 45	Ser 30 Phe	15 Gly Ile	Glu Cys	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 370 <211> 351 <212> DNA <213> Artificial <223> modif. frag.; citrine F1C w. V68L, Q69M mutations <220> <221> CDS <222> (1)..(351) <400> 370 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 tte gge tac gge etq atq tge tte gee ege tac eec gae cac atq aaq 240 Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly 115

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

90

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<210> 371
<211> 117
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; citrine F1C w. V68L, Q69M mutations
<400> 371
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                    10
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                        55
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
Val Lys Phe Glu Gly
        115
<210> 372
<211> 348
<212> DNA
<213> Artificial
<220>
       modif. frag.; citrine F1C w. V68L, Q69M mutations
<223>
       & posit. 1 Met removed
<220>
       CDS
<221>
<222>
       (1)..(348)
<400> 372
gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
               5
                                    10
                                                        15
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc Lys Phe Glu Gly 115	348
<210> 373 <211> 116 <212> PRT <213> Artificial	
<220> <223> modif. frag.; citrine F1C w. V68L, Q69M mutations & posit. 1 Met removed	
<400> 373	
<pre>Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15</pre>	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15  Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25  Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 Lys Phe Glu Gly 115 <210> 374 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1C w. F46L, F64L mutations <220> <221> CDS <222> (1)..(351) <400> 374 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys - 65 egg cac gac tto tto aag tee gec atg eec gaa gge tac gto eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu . 85 90 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly 115

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
        115
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       & posit.1 Met removed
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ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgc Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arc 85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtc Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	
aag ttc gag ggc Lys Phe Glu Gly 115	348
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<pre>&lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; YFP F1C w. F46L, F64L mutations     &amp; posit.1 Met removed  &lt;400&gt; 377  Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val     1</pre>	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 378 <211> 351 <212> DNA <213> Artificial <220> modif. frag.; CFP F1C w. F64L mutation <220> <221> CDS <222> (1)..(351) <400> 378 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 10 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ctc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly 115

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                        55
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
<210> 380
<211> 348
<212> DNA
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<222> (1)..(348)
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
               5
```

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc Lys Phe Glu Gly 115	348
<210> 381 <211> 116 <212> PRT <213> Artificial	
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 382 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C with Y66W mutation <220> <221> CDS <222> (1)..(351) <400> 382 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 75 80 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu . 85 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
               85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
Val Lys Phe Glu Gly
        115
<210>
      384
<211>
       348
<212> DNA
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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gag ctg gac Glu Leu Asp												96
ggc gag ggc Gly Glu Gly 35												144
acc acc ggc Thr Thr Gly 50		Pro V										192
ggc tgg ggc Gly Trp Gly 65												240
cac gac ttc His Asp Phe												288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115												348
<210> 385 <211> 116 <212> PRT <213> Artif	Eicial										·	
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Glu Leu Asp	Gly Asp 20	Val A	Asn Gly	His 25	Lys	Phe	Ser	Val	Ser 30	Gly	Glu	
Gly Glu Gly 35	Asp Ala	Thr 7	Tyr Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Thr Thr Gly 50	Lys Leu		Val Pro 55	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 386 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C with S65A mutation <220> <221> CDS <222> (1)..(351) <400> 386 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 10 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 tte gee tae gge etg eag tge tte gee ege tae eee gae eac atg aag 240 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 ege ace ate tte tte aag gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

85

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<212>
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                                        75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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                                                        95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
Val Lys Phe Glu Gly
        115
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       388
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       348
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      DNA
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                    10
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gag ctg gac Glu Leu Asp												96
ggc gag ggc Gly Glu Gly 35												144
acc acc ggc Thr Thr Gly 50	aag ctg Lys Leu	ccc gtg Pro Vai	g ccc Pro	tgg Trp	ccc Pro	acc Thr	ctc Leu 60	gtg Val	acc Thr	acc Thr	ttc Phe	192
gcc tac ggc Ala Tyr Gly 65					Tyr							240
cac gac ttc His Asp Phe				Pro								288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115												348
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							711 &	F-2-				
Val Ser Lys 1	Gly Glu 5	Glu Lei	Phe		Gly '					Leu 15		
	5		Gly		10	Val	Val	Pro	Ile	15	Val	
1	5 Gly Asp 20	Val Asr	Gly	His : 25	10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	15 Gly	<b>V</b> al Glu	
Glu Leu Asp	5 Gly Asp 20 Asp Ala	Val Asr	Gly Gly 40	His : 25 Lys :	10 Lys : Leu '	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30	15 Gly Ile	<b>V</b> al Glu Cys	

85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 390 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C , S65A, Y66W, and S72A mutations <220> <221> CDS <222> (1)..(351) <400> 390 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gaq 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                  25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                              40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                     70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85 .
                                      90
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
             100
                                  105
Val Lys Phe Glu Gly
        115
<210> 392
<211> 348
<212> DNA
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       modif. frag.; CFP F1C , S65A, Y66W, and S72A mutations
       & posit. 1 Met removed
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                                                                           48
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	ctg ccc gtg ccc tgg Leu Pro Val Pro Trp 55		
	cag tgc ttc gcc cgc Gln Cys Phe Ala Arg 70		
	aag tcc gcc atg ccc Lys Ser Ala Met Pro 85		
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aag ttc gag ggc Lys Phe Glu Gly 115			348
<210> 393 <211> 116 <212> PRT <213> Artificia	al		
	rag.; CFP F1C , S65A, 1 Met removed	Y66W, and S72A muta	ations
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Glu Leu Asp Gly 20	Asp Val Asn Gly His 25	Lys Phe Ser Val Ser 30	Gly Glu
Gly Glu Gly Asp 35	Ala Thr Tyr Gly Lys 40	Leu Thr Leu Lys Phe 45	Ile Cys
Thr Thr Gly Lys 50	Leu Pro Val Pro Trp 55	Pro Thr Leu Val Thr 60	Thr Phe
Ala Trp Gly Leu			i i

85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 394 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C , F64L, S65T, and Y66W mutations <220> <221> CDS <222> (1)..(351) <400> 394 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gto gag otg gac ggo gta aac ggo cac aag tto ago gtg too ggo 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc qac cac atq aaq 240 Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 80 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 ege ace ate tte tte aag gae gae gge aae tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 110 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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<210> 395
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
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       & posit. 1 Met removed
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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gag ctg gac Glu Leu Asp													96
ggc gag ggc Gly Glu Gly 35													144
acc acc ggc Thr Thr Gly 50													192
acc tgg ggc Thr Trp Gly 65													240
cac gac ttc His Asp Phe													288
acc atc ttc Thr Ile Phe													336
aag ttc gag Lys Phe Glu 115													348
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Glu Leu Asp	Gly Asp 20	Val	Asn	Gly	His 25	Lys	Phe	Ser	Val	Ser 30	Gly	Glu	
Gly Glu Gly 35	Asp Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Thr Thr Gly 50	Lys Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Leu	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 398 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1C with Y66H mutation <220> <221> CDS <222> (1)..(351) <400> 398 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 10 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240 Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
               85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
<210> 400
<211> 348
<212> DNA
<213> Artificial
<223> modif. frag.; BFP F1C w. Y66H mutation & posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(348)
<400> 400
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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<210> 399

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acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc Lys Phe Glu Gly 115	348
<210> 401 <211> 116 <212> PRT <213> Artificial	
<220> <223> modif. frag.; BFP F1C w. Y66H mutation & posit. 1 Met remove	d
<400> 401	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 402 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1C w. F64L, Y66H mutations <220> <221> CDS <222> (1)..(351) <400> 402 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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<220>
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
Val Lys Phe Glu Gly
       115
<210> 404
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      348
<212> DNA
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<223> modif. frag.; BFP F1C w. F64L, Y66H mutations
      & posit. 1 Met removed
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<221> CDS
<222> (1)..(348)
<400> 404
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                   10
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	ggc gac Gly Asp 20											96	
ggc gag ggc Gly Glu Gly 35												144	
acc acc ggc Thr Thr Gly 50												192	
ggc cac ggc Gly His Gly 65												240	
cac gac ttc His Asp Phe												288	
acc atc ttc Thr Ile Phe												336	
aag ttc gag Lys Phe Glu 115												348	
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<223> modi	_			F64	.L, Y	'66Н	muta	ition	ıs				
<223> modi	_			. F64	L, Y	'66Н	muta	ution	ıs				
<223> modi & po	sit. 1 M	et remov	red	Thr						Leu 15	Val		
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<223> modi & po: <400> 405  Val Ser Lys 1	Gly Glu 5 Gly Asp 20	et remov Glu Leu Val Asr	red 1 Phe 1 Gly	Thr His 25	Gly 10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	15 Gly	Glu		
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 406 <211> 369 <212> DNA <213> Artificial <220> modif. frag.; YFP F2C and Met added @ position 1 <223> <220> <221> CDS <222> (1)..(369) <223> YFP F2C corresponds to aa residues 118-239 of YFP <400> 406 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 95 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 369 ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

85

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       PRT
       Artificial
 <213>
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 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
                             40
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
     50
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                         75
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                                         95
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
             100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 408
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       366
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       CDS
<221>
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       (1)..(366)
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gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

<210> 407

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 75 80	240
gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20  Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 410 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2C w. Y203F mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 410 atg gac acc ctg gtg aac cgc atc gag ctg aag gqc atc gac ttc aaq 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg caq ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 369 ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115

Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn

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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<210> 412
<211> 366
<212> DNA
<213> Artificial
<223> modif. frag.; YFP F2C with Y203H mutation
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<221> CDS
<222> (1)..(366)
<400> 412
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                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
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gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 75 80	240
gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 413 <211> 122 <212> PRT <213> Artificial	
<220> <223> modif. frag.; YFP F2C with Y203H mutation	
<400> 413	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	
20 25 30  Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	

85 90 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120 <210> 414 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2C w. Y203H mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 414 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 ccc gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn

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<210> 415
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       123
<212>
       PRT
<213>
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<220>
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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
                            40
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                                        95
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210> 416
<211> 366
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; CFP F2C with N146I mutation
<220>
<221> CDS
<222>
       (1)..(366)
       CFP F2C corresponds to residues 118-239 of YFP
<400> 416
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                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
                5
                                    10
                                                        15
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Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 417	
<211> 122 <212> PRT <213> Artificial	
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<212> PRT <213> Artificial  <220> <223> modif. frag.; CFP F2C with N146I mutation	
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<pre>&lt;212&gt; PRT &lt;213&gt; Artificial  &lt;220&gt; &lt;223&gt; modif. frag.; CFP F2C with N146I mutation &lt;400&gt; 417  Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1</pre>	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 418 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 418 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 25 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 55 240 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 75 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

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<210> 419
<211> 123
<212> PRT
<213> Artificial
<220>
<223>
      modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                25
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
                                        75
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
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<211>
       366
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      Artificial
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                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
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gac ggc aac Asp Gly Asn												96	
aac gtc tat Asn Val Tyr 35												144	
ttc aag atc Phe Lys Ile 50	cgc cac Arg His	aac atc Asn Ile 55	gag Glu	gac Asp	ggc Gly	agc Ser	gtg Val 60	cag Gln	ctc Leu	gcc Ala	gac Asp	192	
cac tac cag His Tyr Gln 65												240	
gac aac cac Asp Asn His												288	
gag aag cgc Glu Lys Arg												336	
atc act ctc Ile Thr Leu 115												366	
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Asp Thr Leu 1	Val Asn	Arg Ile	Glu	Len	Laze	<b>-</b>	_	_	_,	T	<b>a</b> 1		
	5			Lea	10	GIY	Ile	Asp	Phe	Lys 15	GIU		
Asp Gly Asn		Gly His	Lys		10			_		15			
Asp Gly Asn Asn Val Tyr 35	Ile Leu 20	_		Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His		
Asn Val Tyr	Ile Leu 20	Ala Asp	Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Val	His Asn		

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 422 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2C w. M153T mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 422 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro . 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
                            40
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
<210> 424
<211> 366
<212> DNA
<213> Artificial
<223> modif. frag.; CFP F2C w. N146I, M153T mutations
<220>
<221> CDS
<222> (1)..(366)
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
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Asp GIY Asi	atc ctg lle Leu 20											96
aac gtc tat Asn Val Tyr 35												144
ttc aag atc Phe Lys Ile 50												192
cac tac cag His Tyr Gli 65												240
gac aac cac Asp Asn His												288
gag aag cgo Glu Lys Aro												336
atc act cto Ile Thr Lev 11!	Gly Met											366
<210> 425 <211> 122	•											
<212> PRT	ficial											
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<212> PRT <213> Art: <220> <223> mod:	f. frag.										Glu	
<212> PRT <213> Art: <220> <223> mod: <400> 425 Asp Thr Lea	f. frag. n Val Asn 5	Arg Il€	e Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15		
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<212> PRT <213> Art: <220> <223> mod: <400> 425  Asp Thr Len 1  Asp Gly Asi Asn Val Tyr	f. frag.  Val Asn  5  Ile Leu 20	Arg Ile	e Glu Lys Lys 40	Leu Leu 25 Gln	Lys 10 Glu Lys	Gly Tyr Asn	Ile Asn Gly	Asp Tyr Ile 45	Phe Ile 30	Lys 15 Ser Val	His Asn	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 426 <211> 369 <212> DNA <213> Artificial <220> modif. frag.; CFP F2C w. N146I, M153T mutations <223> and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 96 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac ttc aag atc cgc cac aac atc gag gac ggc agc gtq caq ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

120

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 <211> 123
 <212> PRT
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       and Met added @ posit. 1
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 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
           100
                                 105
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
· <210> 428
 <211> 366
 <212> DNA
 <213> Artificial
 <220>
 <223> modif. frag.; CFP F2C with V163A mutation
 <220>
 <221> CDS
 <222>
      (1)..(366)
 <400> 428
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
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Asp Gly Asn Ile Leu (	Gly His Lys		aac tac aac Asn Tyr Asn 30													
aac gtc tat atc atg of Asn Val Tyr Ile Met A																
ttc aag atc cgc cac a Phe Lys Ile Arg His A 50																
cac tac cag cag aac a His Tyr Gln Gln Asn 5	acc ccc atc Thr Pro Ile 70	ggc gac ggc Gly Asp Gly 75	ccc gtg ctg Pro Val Leu	ctg ccc 240 Leu Pro 80												
gac aac cac tac ctg a Asp Asn His Tyr Leu 8 85																
gag aag cgc gat cac a Glu Lys Arg Asp His N 100	Met Val Leu															
atc act ctc ggc atg of Ile Thr Leu Gly Met 1115				366												
115 120  <210> 429 <211> 122 <212> PRT <213> Artificial																
<220> <223> modif. frag.;	CFP F2C wit	h V163A mut	<220>													
			acton													
<400> 429			acton													
400> 429 Asp Thr Leu Val Asn A	Arg Ile Glu	Leu Lys Gly 10		Lys Glu 15												
Asp Thr Leu Val Asn A	Gly His Lys :	10	Ile Asp Phe	15												
Asp Thr Leu Val Asn A  Asp Gly Asn Ile Leu C	Gly His Lys :	10 Leu Glu Tyr 25	Ile Asp Phe Asn Tyr Asn 30	15 Ser His												
Asp Thr Leu Val Asn Ash Asp Gly Asn Ile Leu Can Asn Val Tyr Ile Met A	Gly His Lys : : Ala Asp Lys ( 40	Leu Glu Tyr 25 Gln Lys Asn Asp Gly Ser	Ile Asp Phe Asn Tyr Asn 30 Gly Ile Lys 45	15 Ser His Ala Asn												

85 90 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 430 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2C w. V163A mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 430 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 96 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120 <210> 431

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

<211> 123

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 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
                                 25
                                                     30
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                 85
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
         115
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 <211> 366
 <212> DNA
 <213> Artificial
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       CDS
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       (1)..(366)
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 gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                       48
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
                                     10
 gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac
                                                                       96
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
```

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 433 <211> 122 <212> PRT <213> Artificial	
<220> <223> modif. frag.: CFP F2C w. N146I. V163A mutations	
<220> <223> modif. frag.; CFP F2C w. N146I, V163A mutations <400> 433	
<223> modif. frag.; CFP F2C w. N146I, V163A mutations	
<223> modif. frag.; CFP F2C w. N146I, V163A mutations <400> 433 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
<223> modif. frag.; CFP F2C w. N146I, V163A mutations  <400> 433  Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
<pre>&lt;223&gt; modif. frag.; CFP F2C w. N146I, V163A mutations &lt;400&gt; 433  Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1</pre>	
<pre>&lt;223&gt; modif. frag.; CFP F2C w. N146I, V163A mutations &lt;400&gt; 433  Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1</pre>	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110

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<212> DNA
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<213>
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      Met added @ posit. 1
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<221> CDS
<222> (1)..(369)
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                                                                      192
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                                      369
ggg atc act ctc ggc atg gac gag ctg tac aag
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210> 435
<211>
      123
<212>
      PRT
<213> Artificial
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<223>
      modif. frag.; CFP F2C w. N146I, V163A mutations and
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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

Met added @ posit. 1

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G	Hu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Ile	Ser	
ŀ	His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
F	Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
	Asp 55	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
E	Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
P	Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
9	Sly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
<	210 211 212 213	L> . 2> 1	136 366 ONA Artii	ficia	al												
	:220 :223		modii	E. fi	rag.	; CFI	P F20	C w.	M153	3T, V	/163/	A mi	ıtati	ions			
<	:220 :221 :222	L> (	CDS (1).	. (366	5)												
ç	jac Asp	acc				cgc Arg											48
						ggg Gly											96

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45

ttc aag atc Phe Lys Ile 50			le Glu									192
cac tac cag His Tyr Glr 65												240
gac aac cac Asp Asn His												288
gag aag cgc Glu Lys Arg												336
atc act ctc Ile Thr Leu 115	Gly Met		-		-							366
<210> 437 <211> 122 <212> PRT <213> Arti	ficial											
<220> <223> modi	f. frag.	; CFP 1	F2C w.	M153	3T, V	7163 <i>F</i>	A mi	ıtati	lons			
<400> 437												
<400> 437 Asp Thr Leu 1	Val Asn 5	Arg I	le Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp Thr Leu	5				10	-				15		
Asp Thr Leu	5 Ile Leu 20	Gly H	is Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp Thr Leu 1 Asp Gly Asn Asn Val Tyr	Ile Leu 20	Gly H	is Lys  Sp Lys  40  le Glu	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp Thr Leu  Asp Gly Asn  Asn Val Tyr  35  Phe Lys Ile	Ile Leu 20 Ile Thr	Gly H: Ala As Asn I:	is Lys  Ep Lys  40  le Glu	Leu 25 Gln Asp	10 Glu Lys Gly	Tyr Asn Ser	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	15 Ser Ala	His Asn Asp	
Asp Thr Leu 1  Asp Gly Asn  Asn Val Tyr 35  Phe Lys Ile 50  His Tyr Gln	Ile Leu 20 Ile Thr Arg His	Gly H: Ala As Asn II 55	is Lys  EXP  EXP  EXP  EXP  EXP  EXP  EXP  EX	Leu 25 Gln Asp	10 Glu Lys Gly Asp	Tyr Asn Ser Gly 75	Asn Gly Val 60	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	15 Ser Ala Ala	His Asn Asp Pro 80	

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<210> 438
<211> 369
<212> DNA
<213> Artificial
<220>
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       and Met added @ posit. 1
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc acc gcc gac aag cag aac ggc atc aag gcc
                                                                     144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                        75
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                     288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
                                105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                     369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
                            120
<210> 439
<211> 123
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<220>
<223> modif. frag.; CFP F2C w. M153T, V163A mutations
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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

and Met added @ posit. 1

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Met 1	Asp	Thr	Leu	Val 5	Asn	Arg	Ile	Glu	Leu 10	Lys	Gly	Ile	Asp	Phe 15	Lys	
Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											48
					ggg Gly											96

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ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 10 Leu Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 30  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 40  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 30  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 45  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50  His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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115
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                 25
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                       144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35
                             40
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                         55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                       240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                       288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                       336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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                                 105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                       369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Ile	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc	444 ctg Leu														48

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac

Asn Val Tyr 35	Ile Thr	Ala As	sp Lys 40	Gln	Lys	Asn	Gly	Ile 45	Lys	Val	Asn	
ttc aag atc Phe Lys Ile 50			le Glu									192
cac tac cag His Tyr Gln 65												240
gac aac cac Asp Asn His												288
gag aag cgc Glu Lys Arg												336
atc act ctc Ile Thr Leu 115	Gly Met											366
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•										Lys 15	Glu	
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<pre>&lt;400&gt; 445 Asp Thr Leu 1 Asp Gly Asn Asn Val Tyr 35</pre>	Val Asn 5 Ile Leu 20 Ile Thr	Arg II	le Glu is Lys Ep Lys 40	Leu Leu 25 Gln Asp	Lys 10 Glu Lys	Gly Tyr Asn Ser	Ile Asn Gly Val	Asp Tyr Ile 45 Gln	Phe Asn 30 Lys	15 Ser Val	His Asn Asp	
<pre>&lt;400&gt; 445 Asp Thr Leu 1 Asp Gly Asn Asn Val Tyr 35 Phe Lys Ile 50 His Tyr Gln</pre>	Val Asn 5  Ile Leu 20  Ile Thr  Arg His	Arg II Gly H: Ala As Asn II 55 Thr Pr 70	le Glu is Lys Ep Lys 40 le Glu co Ile	Leu Leu 25 Gln Asp	Lys 10 Glu Lys Gly	Gly Tyr Asn Ser Gly 75	Ile Asn Gly Val 60	Asp Tyr Ile 45 Gln Val	Phe Asn 30 Lys Leu Leu	Ser Val Ala	His Asn Asp Pro 80	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg age tac cag tcc gcc ctg age aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                     110
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
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120

115

Met added @ posit. 1

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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											48
					999											96

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ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20  Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20  Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 30  Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Asn 55  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 55  His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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115
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       450
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                        96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                       144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                       240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                       288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                       336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                     110
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                       369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
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      123
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      PRT
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      Artificial
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Île	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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					Gly 999											91
					gcc Ala											144

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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1 5 10 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Asn Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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       369
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       Artificial
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       and Met added @ posit. 1
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20
                                25
cac aac gtc tat atc acc gcc gac aag cag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
                            40
                                                                      192
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                                                      288
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                                      369
ggg atc act ctc ggc atg gac gag ctg tac aag
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
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His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											48
gac	ggc	aac	atc	ctg	999	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	96

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

. 35		40	45
ttc aag atc c		gag gac ggc agc gtg Glu Asp Gly Ser Val	cag ctc gcc gac 192
		atc ggc gac ggc ccc Ile Gly Asp Gly Pro 75	
		cag tcc gcc ctg ago Gln Ser Ala Leu Ser 90	
Glu Lys Arg A		ctg ctg gag ttc gtg Leu Leu Glu Phe Val 105	
	ggc atg gac gag Gly Met Asp Glu		366
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	Tle Leu Gly His 20	Lys Leu Glu Tyr Asn 25	Tyr Asn Ser His 30
Asn Val Tyr I 35	lle Thr Ala Asp	Lys Gln Lys Asn Gly	Ile Lys Ala Asn 45
Phe Lys Ile A	Arg His Asn Ile 55	Glu Asp Gly Ser Val	Gln Leu Ala Asp
His Tyr Gln G 65	Sln Asn Thr Pro 70	Ile Gly Asp Gly Pro	Val Leu Leu Pro 80

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110

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115
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20
                                25
cac aac gtc tat atc acc gcc gac aag cag aag aac gqc atc aag qcc
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arq His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65
                                         75
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                    90
                                                         95
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys					·	
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	acc	160 ctg Leu														48
		aac Asn														9
		tat Tyr 35														144

					aac Asn											192
					acc Thr 70											240
					agc Ser											288
					atg Met											336
					gac Asp		_		_							366
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	١.															
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	3> r	nodif 161	E. f1	rag.;	; CGI	FP F2	2C, 1	N146:	[, M:	L53T,	, V16	53A,	and	1203	3Y mutatio	ons
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       and Met added @ posit. 1
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
                5
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                25
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                    90
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arq Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Ile	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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					espor	nds t	to aa	a res	sidue	es 13	18-23	39 of	E YFI	ē		
gac	0> 4 acc Thr	ctg														48
	ggc															96

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn

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		gag gac ggc agc gtg Glu Asp Gly Ser Va: 60	
		atc ggc gac ggc ccc Ile Gly Asp Gly Pro 75	
		cag tcc gcc ctg ago Gln Ser Ala Leu Ser 90	
		ctg ctg gag ttc gtg Leu Leu Glu Phe Va 105	
atc act ctc ggc Ile Thr Leu Gly 115	Met Asp Glu		366
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<223> modif. f	rug., bii izc	w. 1143F mucacion	
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<pre>&lt;400&gt; 465  Asp Thr Leu Val 1  Asp Gly Asn Ile 20  Asn Val Tyr Ile 35</pre>	Asn Arg Ile of 5  Leu Gly His Met Ala Asp	Glu Leu Lys Gly Ile 10 Lys Leu Glu Tyr Asn 25 Lys Gln Lys Asn Gly	15 n Phe Asn Ser His 30 y Ile Lys Val Asn 45
<pre>&lt;400&gt; 465  Asp Thr Leu Val 1  Asp Gly Asn Ile 20  Asn Val Tyr Ile 35  Phe Lys Ile Arg 50</pre>	Asn Arg Ile of 5  Leu Gly His Met Ala Asp His Asn Ile of 55	Glu Leu Lys Gly Ile 10 Lys Leu Glu Tyr Asr 25 Lys Gln Lys Asn Gly 40 Glu Asp Gly Ser Val	15 n Phe Asn Ser His 30 y Ile Lys Val Asn 45 l Gln Leu Ala Asp

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser
                                                                      144
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65
                                         75
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                                         95
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                 105
                                                                      369
ggg atc act ctc ggc atg gac gag ctg tac aag
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Phe 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	.> !>	CDS (1). Venus			rresi	ponds	s to	aa 1	cesio	dues	118-	-239	of Y	/FP		
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn

		35					40				•	45				
		atc			aac		gag					cag				192
	50		_		Asn	55		_	_		60				-	
					acc Thr 70											240
					agc Ser											288
					atg Met											336
					gac Asp											366
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Asp 1	Thr	Leu	Val	Asn 5	Arg	Ile	Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp	Gly	Asn	Ile 20	Leu	Gly	His	Lys	Leu 25	Glu	Tyr	Asn	Tyr	Asn 30	Ser	His	
Asn	Val	Tyr 35	Ile	Met	Ala	Asp	Lys 40	Gln	Lys	Asn	Gly	Ile 45	Lys	Val	Asn	
Phe	Lys 50	Ile	Arg	His	Asn	Ile 55	Glu	Asp	Gly	Gly	Val 60	Gln	Leu	Ala	Asp	
His 65	Tyr	Gln	Gln	Asn	Thr 70	Pro	Ile	Gly	Asp	Gly 75	Pro	Val	Leu	Leu	Pro 80	
Asp	Asn	His	Tyr	Leu 85	Ser	Tyr	Gln	Ser	Ala 90	Leu	Ser	Lys	Asp	Pro 95	Asn	
Glu	Lys	Arg	Asp 100	His	Met	Val	Leu	Leu 105	Glu	Phe	Val	Thr	Ala 110	Ala	Gly	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20
                                25
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg
                                                                     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc qcc gcc
                                                                     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
           100
                                105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                     369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu As	o Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His As	n Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn Pho	e Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp Hi	s Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro As	) Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn Gl	ı Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly Ile	e Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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144

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aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  50  55  60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15  Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 30  Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35  Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp 50  His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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       and Met added @ posit. 1
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
                                25
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                        75
ccc gac aac cac tac ctg agc tac cag tcc qcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
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                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn Phe	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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144

30

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

25

Pne	aag Lys 50															192
	tac Tyr															240
	aac Asn															288
	aag Lys															336
	act Thr			_	_		_		_							366
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Asp 1		Leu		5	_				10	-		_		15		
Asp 1 Asp	Thr	Leu Asn	Ile 20	5 Leu	Gly	His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp 1 Asp	Thr	Leu Asn Tyr 35	Ile 20	5 Leu Met	Gly	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp 1 Asp Asn	Thr Gly Val	Leu Asn Tyr 35	Ile 20 Ile Arg	Leu Met	Gly Ala Asn	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly	Tyr Asn Gly	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	15 Ser Ala Ala	His Asn Asp	
Asp 1 Asp Asn Phe	Thr Gly Val	Leu Asn Tyr 35 Ile Gln	Ile 20 Ile Arg	Leu Met His	Gly Ala Asn Thr	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly Asp	Tyr Asn Gly Gly 75	Asn Gly Val 60 Pro	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	Ser Ala Ala Leu	His Asn Asp Pro 80	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
                                25
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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                                105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                     369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											48
					gly ggg											90
					gcc Ala											144

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cac ta His Ty 65	c cag r Gln	cag Gln	aac Asn	acc Thr 70	ccc Pro	atc Ile	ggc Gly	gac Asp	ggc Gly 75	ccc Pro	gtg Val	ctg Leu	ctg Leu	CCC Pro 80	240
gac aa Asp As															288
gag aa Glu Ly															336
atc ac Ile Th			_	_		_		_							366
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Asp Th	r Leu		5					10					15		
Asp Th	r Leu y Asn	Ile 20	5 Leu	Gly	His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp Th	y Asn Tyr 35	Ile 20	5 Leu Thr	Gly Ala	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp The last Asp Gl Asn Va	y Asn 1 Tyr 35	Ile 20 Ile Arg	5 Leu Thr	Gly Ala Asn	His Asp Ile 55	Lys Lys 40	Leu 25 Gln Asp	10 Glu Lys Gly	Tyr Asn Gly	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	Ser Ala Ala	His Asn Asp	
Asp The last section of th	y Asn 1 Tyr 35 s Ile	Ile 20 Ile Arg	5 Leu Thr His	Gly Ala Asn Thr	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly Asp	Tyr Asn Gly Gly 75	Asn Gly Val 60 Pro	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	Ser Ala Ala Leu	Asn Asp Pro 80	

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 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                         96
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                        144
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
         35
                                                  45
 aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                        192
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Val Gln Leu Ala
     50
                          55
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                        240
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65
                                          75
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                        288
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                 85
                                                          95
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                        336
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
             100
                                  105
                                                      110
 ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                        369
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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modif. frag.; Venus F2C, M153T, V163A, and S175G mutations

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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

<210> 484 <211> 471

<212> DNA

<213> Artificial

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<223> modif. frag.; YFP F1DX w. position 1 Met removed

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<221> CDS

<222> (1)..(471)

<223> YFP F1DX fragment corresponds to aa residues 1-158 of YFP

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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 14

	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
					ccc Pro											192
					tgc Cys 70											240
					tcc Ser											288
					gac Asp											336
					acc Thr											384
					ggc Gly											432
					gtc Val 150											471
<210 <210 <210 <210	l> : 2> :	185 157 PRT Artif	Eicia	al												
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<213 <213 <213 <220	1 > 2   1   3   3   3   4   3   5   5   5   5   5   5   5   5   5	l57 PRT Artif			. YFI	? F1I	OX w.	. pos	sitio	on 1	Met	remo	oved			
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<21: <21: <21: <22: <40: Val	1> 1 2> 1 3> <i>h</i> 0> 3> r 0> 4	L57 PRT Artif Modif Lys	f. fr	rag.; Glu 5		Leu	Phe	Thr	Gly 10	Val	Val	Pro	Ile	15		
<21: <21: <21: <22: <40:  Val  Glu	1> : 2> I 3> / 3> / 3> / 0> Ser	L57 PRT Artif Modif Lys Asp	Gly Gly 20	Glu 5 Asp	Glu	Leu Asn	Phe Gly	Thr His 25	Gly 10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	15 Gly	Glu	
<21: <21: <22: <22: <40:  Val  Glu  Gly	1 > : : : : : : : : : : : : : : : : : :	Asp Gly 35	Gly Gly 20 Asp	Glu 5 Asp	Glu Val	Leu Asn Tyr	Phe Gly Gly 40	Thr His 25	Gly 10 Lys	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30	15 Gly Ile	Glu Cys	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 486 <211> 474 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1DX with K79R mutation <220> <221> CDS <222> (1)..(474) <400> 486 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tto ggo tac ggo ctg cag tgo tto goo cgo tac coc gac cac atg aag 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 80 288 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gaq 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110
gtg aag ttc gag ggc gac acc ctg Val Lys Phe Glu Gly Asp Thr Leu 115	Val Asn Arg Ile Glu	
atc gac ttc aag gag gac ggc aac Ile Asp Phe Lys Glu Asp Gly Asr 130		
aac tac aac agc cac aac gtc tat Asn Tyr Asn Ser His Asn Val Tyr 145		
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Val Glu Leu Asp Gly Asp Val Asr 20	Gly His Lys Phe Ser 25	Val Ser Gly 30
Glu Gly Glu Gly Asp Ala Thr Tyr 35 40	Gly Lys Leu Thr Leu 45	Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val	Pro Trp Pro Thr Leu	Val Thr Thr
Phe Gly Tyr Gly Leu Gln Cys Phe	Ala Arg Tyr Pro Asp 75	His Met Lys 80
Arg His Asp Phe Phe Lys Ser Ala	Met Pro Glu Gly Tyr 90	Val Gln Glu 95
Arg Thr Ile Phe Phe Lys Asp Asp	Gly Asn Tyr Lys Thr	Arg Ala Glu 110
Val Lys Phe Glu Gly Asp Thr Leu 115 120		Leu Lys Gly
Ile Asp Phe Lys Glu Asp Gly Asn 130 135	Ile Leu Gly His Lys 140	Leu Glu Tyr

<210> 488 <211> 471 <212> DNA Artificial <213> <220> <223> modif. frag.; YFP F1DX, w. K79R mutation, and posit. 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 488 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

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<212> PRT
<213> Artificial
<220>
removed
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<223> modif. frag.; YFP F1DX, w. K79R mutation, and posit. 1 Met

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 70

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 120

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150

<210> 490

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX with Y66F mutation

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                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tto ggc tto ggc ctg cag tgc tto gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag
                                                                     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
                                                                     474
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
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      158
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 70 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu 85 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 . Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 492 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 492 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc aqc qtg tcc ggc qaq 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ggc gag ggc gat gcc acc tac ggc aaq ctq acc ctq aaq ttc atc tqc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

50	aag ctg Lys Leu	Pro V										192
ggc ttc ggc Gly Phe Gly 65												240
cac gac ttc His Asp Phe				Pro.								288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115					_			_	_			384
gac ttc aag Asp Phe Lys 130		Gly A						Leu				432
tac aac agc Tyr Asn Ser 145											·	471
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	-			Thr								ed
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 494 <211> 474 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1DX with Q69K mutation <220> <221> CDS <222> (1)..(474) <400> 494 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc qqc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tto ggo tac ggo otg aag tgo tto goo ogo tac ooc qac cac atg aag 240 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

				100					105					110			
							acc Thr										384
							ggc Gly 135										432
i							gtc Val										474
	<21( <211 <212 <213	L> 1 2> I	195 158 PRT Artii	Eicia	al												
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	<400	)> 4	195														
	Met 1	Val	Ser	Lys	Gly 5	Glu	Glu	Leu	Phe	Thr 10	Gly	Val	Val	Pro	Ile 15	Leu	
7	Val	Glu	Leu	Asp 20	Gly	Asp	Val	Asn	Gly 25	His	Lys	Phe	Ser	Val 30	Ser	Gly	
(	3lu	Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile	
(	Cys	Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr	
	Phe 65	Gly	Tyr	Gly	Leu	Lys 70	Cys	Phe	Ala	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80	
ī	Arg	His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu	
I	Arg	Thr	Ile	Phe 100	Phe	Lys	Asp	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu	
,	Val	Lys	Phe 115	Glu	Gly	Asp	Thr	Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly	
•	Ile	Asp 130	Phe	Lys	Glu	Asp	Gly 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr	

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155
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gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc  Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60
ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg  Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  100  105  110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag  Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  145  150  155

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<220>

<223> modif. frag.; YFP F1DX, Q69K mutation, and posit. 1 Met removed

<400> 497

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155

<210> 498

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1DX with V68L, Q69M mutations

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
tto ggo tac ggo otg atg tgo tto goo ogo tac occ gao cac atg aag
                                                                      240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
                                         75
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130
                        135
                                                                      474
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
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<213>
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<220>
<223>
      modif. frag.; citrine F1DX with V68L, Q69M mutations
<400>
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 120 115 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 500 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; citrine F1DX, V68L and Q69M mutations, and position 1 Met removed <220> <221> CDS (1)..(471) <222> <400> 500 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 5 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25

ggc gag ggc gat gcc acc tac ggc aag ctg acc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40	• •
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55	
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro 75	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90	
acc atc ttc ttc aag gac gac ggc aac tac aag Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105	
aag ttc gag ggc gac acc ctg gtg aac cgc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120	
gac ttc aag gag gac ggc aac atc ctg ggg cac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130	
tac aac agc cac aac gtc tat atc atg gcc gac Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145	
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25	Ser Val Ser Gly Glu 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40	Leu Lys Phe Ile Cys 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	Leu Val Thr Thr Phe

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	
<210> 502 <211> 474 <212> DNA <213> Artificial	
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<223> modif. frag.; CFP F1DX with F64L mutation  <220> <221> CDS <222> (1)(474)  <400> 502	48
<pre>&lt;223&gt; modif. frag.; CFP F1DX with F64L mutation  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(474)  &lt;400&gt; 502 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15</pre>	48
<pre>&lt;223&gt; modif. frag.; CFP F1DX with F64L mutation  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(474)  &lt;400&gt; 502 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	
<pre>&lt;223&gt; modif. frag.; CFP F1DX with F64L mutation  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(474)  &lt;400&gt; 502 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	96
<pre>&lt;223&gt; modif. frag.; CFP F1DX with F64L mutation  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(474)  &lt;400&gt; 502 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	96 44

	85	90	95
	ttc aag gac gac ggc Phe Lys Asp Asp Gly 105		
	ggc gac acc ctg gtg Gly Asp Thr Leu Val 120		
	gag gac ggc aac atc Glu Asp Gly Asn Ile 135		
	cac aac gtc tat atc His Asn Val Tyr Ile 150		474
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<400> 503			
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Val Glu Leu Asp 20	Gly Asp Val Asn Gly 25	His Lys Phe Ser Val	Ser Gly
Glu Gly Glu Gly	Asp Ala Thr Tyr Gly	Lys Leu Thr Leu Lys 45	Phe Ile
Cys Thr Thr Gly	Lys Leu Pro Val Pro 55	Trp Pro Thr Leu Val	Thr Thr
Leu Gly Tyr Gly 65	Leu Gln Cys Phe Ala 70	Arg Tyr Pro Asp His	Met Lys 80
Arg His Asp Phe	Phe Lvs Ser Ala Met	Due Gla Gla H a Mal	Gln Glu
	85	90	95

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln
145					150					155			

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gag ct Glu Le															96
ggc ga Gly Gl															144
acc ac Thr Th 50															192
ggc ta Gly Ty 65															240
cac ga His As															288
acc at Thr Il															336
aag tt Lys Ph															384
gac tt Asp Ph 13	e Lys														432
tac aa Tyr As															471

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                    70
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130
                        135
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145
                    150
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       506
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       474
<212>
       DNA
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       Artificial
<220>
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Cys Thr T 50	Thr Gly	Lys Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr		
Leu Thr I 65	Trp Gly	Leu Gln 70	Cys	Phe	Ala	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80		
Arg His A	Asp Phe	Phe Lys 85	Ser .	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu		
Arg Thr I	Ile Phe 100	Phe Lys	Asp .	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu		
Val Lys P	Phe Glu	Gly Asp		Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly		
Ile Asp P 130	Phe Lys	Glu Asp	Gly . 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr		
Asn Tyr A 145	Asn Ser	His Asn 150		Tyr	Ile	Met	Ala 155	Asp	Lys	Gln				
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		rag.; CF				S65	БТ, а	and Y		muta	ation	ıs,		
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ggc gag g	gc gat	gcc acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	:	144

	Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
										ccc Pro							192
										tac Tyr							240
										gaa Glu 90							288
										tac Tyr							336
										cgc Arg							384
										gly ggg							432
										gcc Ala							471
	<210 <211 <212 <213	.> 1 ?> E	509 L57 PRT Artif	ficia	al												
	<220 <223	3 > n						OX F									
				,	.1011	T ME	et re	emove		. S65	5T, a	and Y	766W	muta	atior	ıs,	
	<400	)> 5	509		.1011	1 ME	et re			. S65	5T, ā	and Y	766W	muta	ation	ıs,	
								emove	ed	Gly 10							
	Val 1	Ser	Lys	Gly	Glu 5	Glu	Leu	Phe	ed Thr	Gly	Val	Val	Pro	Ile	Leu 15	Val	
-	Val 1 Glu	Ser	Lys Asp	Gly Gly 20	Glu 5 Asp	Glu Val	Leu Asn	Phe Gly	Thr His 25	Gly 10	Val Phe	Val Ser	Pro Val	Ile Ser	Leu 15 Gly	Val Glu	
	Val 1 Glu Gly	Ser Leu Glu	Lys Asp Gly 35	Gly Gly 20	Glu 5 Asp Ala	Glu Val Thr	Leu Asn Tyr	Phe Gly Gly 40	Thr His 25 Lys	Gly 10 Lys	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30	Leu 15 Gly Ile	Val Glu Cys	

 65
 70
 75
 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 510 <211> 474 <212> DNA <213> Artificial <223> modif. frag.; CFP F1DX with Y66W mutation <220> <221> CDS <222> (1)..(474) <400> 510 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tte gge tgg gge etg cag tge tte gee ege tae eee gae cae atg aag 240 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	474
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	

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Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

150

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50
                        55
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                    70
                                        75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
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                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                             40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                        55
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
                                    90
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115
                             120
ate gae tte aag gag gae gge aac ate etg ggg cae aag etg gag tae
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag
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Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys
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20	25	30

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

40

35

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc ac Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Th 50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aa Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Ly 65 70 75	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag ga His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Gl 85 90 95	u Arg
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc ga Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Gl	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag gg Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gl 115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag ta Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Ty 130 135 140	
tac atc agc cac aac gtc tat atc atg gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471
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20 25 30  Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Il	e Cys

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln <210> 518 <211> 474 <212> DNA <213> Artificial <220> modif. frag.; CFP F1DX w. Y66W, M153T mutations <223> <220> <221> CDS <222> (1)...(474)<400> 518 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

			·	
100		105	110	
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		atc acc gcc gac a lle Thr Ala Asp 1 155		474
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Val Glu Leu Asp 20	Gly Asp Val Asn	Gly His Lys Phe 8	Ser Val Ser Gl 30	Y
Glu Gly Glu Gly 35	Asp Ala Thr Tyr	Gly Lys Leu Thr I	Leu Lys Phe Il 45	.e
Cys Thr Thr Gly	Lys Leu Pro Val 55	Pro Trp Pro Thr I	Leu Val Thr Th	nr .
Phe Gly Trp Gly 65	Leu Gln Cys Phe	Ala Arg Tyr Pro A	Asp His Met Ly 80	
Arg His Asp Phe	Phe Lys Ser Ala 85	Met Pro Glu Gly 7	Tyr Val Gln Gl 95	u
Arg Thr Ile Phe	Phe Lys Asp Asp	Gly Asn Tyr Lys 1	Thr Arg Ala Gl	.u

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

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ggc tgg ggc ctg Gly Trp Gly Leu 65				
cac gac ttc ttc His Asp Phe Phe			Tyr Val Gln (	
acc atc ttc ttc Thr Ile Phe Phe 100				
aag ttc gag ggc Lys Phe Glu Gly 115	Asp Thr Leu V			
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Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln

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 posit. 1 Met removed

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

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<213> Artificial

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                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tte gge tae gge etg eag tge tte gee ege tae eee gae eae atg aag
                                                                      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
egg cac gae the the aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag
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Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

35 40 45

50 55 60	192
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cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac atc agc cac aac gtc tat atc atg gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471
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<pre>&lt;220&gt; &lt;223&gt; modif. frag.; CFP F1DX w. N146I mutation, and posit. 1 Met removed &lt;400&gt; 525  Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1</pre>	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 120 115 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 526 <211> 474 <212> DNA <213> Artificial <220> modif. frag.; CFP F1DX with M153T mutation <223> <220> <221> CDS <222> (1)..(474) <400> 526 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu 85 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110

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atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	474
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	

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	agc	528 aag Lys														. 4	8
		gac Asp														9	6
		ggc Gly 35														14	4
		ggc Gly													ttc Phe	19	2
		ggc Gly														24	0
		ttc Phe														28	8
acc Thr	atc Ile	ttc Phe	ttc Phe 100	aag Lys	gac Asp	gac Asp	ggc Gly	aac Asn 105	tac Tyr	aag Lys	acc Thr	cgc Arg	gcc Ala 110	gag Glu	gtg Val	33	6
		gag Glu 115														38	4
		aag Lys														43	2
		agc Ser														47	1

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln

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       modif. frag.; CFP F1DX w. M153T mutation, and posit. 1
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 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                 25
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                                         75
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                 85
                                     90
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
             100
                                 105
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
                             120
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
     130
                         135
                                             140
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145
                     150
 <210> 530
 <211>
       474
 <212> DNA
 <213> Artificial
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<223> modif. frag.; CFP F1DX w. N146I, M153T mutations

<220>

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<222>
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tte gge tae gge etg eag tge tte gee ege tae eee gae eae atg aag
                                                                     240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag
                                                                     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
aac tac atc aqc cac aac qtc tat atc acc qcc qac aaq caq
                                                                     474
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
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<211> 158
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      modif. frag.; CFP F1DX w. N146I, M153T mutations
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 150 <210> 532 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1DX, N146I, M153T mutations, and posit. 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 532 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tqc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Pho 50 55 60	192 e
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgc Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtc Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asr 130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	471
<210> 533 <211> 157 <212> PRT	
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<2213> Artificial  <220> <223> modif. frag.; CFP F1DX, N146I, M153T mutations, and post Met removed	it. 1
<220> <223> modif. frag.; CFP F1DX, N146I, M153T mutations, and pos	it. 1
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<pre>&lt;220&gt; &lt;223&gt; modif. frag.; CFP F1DX, N146I, M153T mutations, and post</pre>	L
<pre>&lt;220&gt; &lt;223&gt; modif. frag.; CFP F1DX, N146I, M153T mutations, and post Met removed  &lt;400&gt; 533  Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1</pre>	L 1
<pre>&lt;220&gt; &lt;223&gt; modif. frag.; CFP F1DX, N146I, M153T mutations, and post Met removed  &lt;400&gt; 533  Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1</pre>	l L

His Asp Phe Phe Lys Ser Ala Met Pi 85	Pro Glu Gly Tyr Val Gln Glu Arg 90 95
Thr Ile Phe Phe Lys Asp Asp Gly As	asn Tyr Lys Thr Arg Ala Glu Val .05 110
Lys Phe Glu Gly Asp Thr Leu Val As	asn Arg Ile Glu Leu Lys Gly Ile 125
Asp Phe Lys Glu Asp Gly Asn Ile Le	eu Gly His Lys Leu Glu Tyr Asn 140
Tyr Ile Ser His Asn Val Tyr Ile Th 145 150	Thr Ala Asp Lys Gln 155
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<pre>&lt;222&gt; (1)(474)  &lt;400&gt; 534 atg gtg agc aag ggc gag gag ctg tt Met Val Ser Lys Gly Glu Glu Leu Pt 1</pre>	The Thr Gly Val Val Pro Ile Leu 10 15  ggc cac aag ttc agc gtg tcc ggc 96 Gly His Lys Phe Ser Val Ser Gly 30  ggc aag ctg acc ctg aag ttc atc Gly Lys Leu Thr Leu Lys Phe Ile 45  gcc tgg ccc acc ctc gtg acc acc 192
<pre>&lt;222&gt; (1)(474)  &lt;400&gt; 534 atg gtg agc aag ggc gag gag ctg tt Met Val Ser Lys Gly Glu Glu Leu Pt 1</pre>	The Thr Gly Val Val Pro Ile Leu 10 15  ggc cac aag ttc agc gtg tcc ggc 96 Gly His Lys Phe Ser Val Ser Gly 30  ggc aag ctg acc ctg aag ttc atc 144 Gly Lys Leu Thr Leu Lys Phe Ile 45  gcc tgg ccc acc ctc gtg acc acc 200 Trp Pro Thr Leu Val Thr Thr 60  gcc cgc tac ccc gac cac atg aag 240
<pre>&lt;222&gt; (1)(474)  &lt;400&gt; 534 atg gtg agc aag ggc gag gag ctg tt Met Val Ser Lys Gly Glu Glu Leu Ph 1</pre>	The Thr Gly Val Val Pro Ile Leu 10 15  ggc cac aag ttc agc gtg tcc ggc 96  gly His Lys Phe Ser Val Ser Gly 30  ggc aag ctg acc ctg aag ttc atc 144  gly Lys Leu Thr Leu Lys Phe Ile 45  gcc tgg ccc acc ctc gtg acc acc 192  gcc tgg ccc acc ctc gtg acc acc 192  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc cgc tac ccc gac cac atg aag 240  gcc ccc gaa ggc tac gtc cag gag 288